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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 00:31:06 ; Search time 2252 Seconds

(without alignments)
2167.848 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 aatgcctgcacgaactcct.....ttttagaacaagaagaaga 963

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	963	100.0	963	15	US-10-023-597-23
2	755.4	78.4	931	15	US-10-017-161-1301
3	755.4	78.4	931	16	US-10-292-798-1069
4	694.2	72.1	1333	15	US-10-017-161-325
5	694.2	72.1	1333	16	US-10-292-798-291
6	693	72.0	976	15	US-10-024-399-1
7	692.4	71.9	953	16	US-10-005-041R-13
8	691.6	71.8	933	9	US-08-886-055-50
9	691.6	71.8	933	10	US-09-804-291-50
10	691.6	71.8	933	13	US-10-343-650A-395
11	691.6	71.8	933	15	US-10-220-382-35
12	657.4	68.3	1336	15	US-10-017-161-749
13	657.4	68.3	1336	16	US-10-292-798-653
14	650.6	67.6	942	13	US-10-343-650A-397

15	650.6	67.6	951	16	US-10-387-629-47	Sequence 47, App1
16	649.6	67.5	936	15	US-10-220-382-36	Sequence 36, App1
17	554.8	57.6	886	15	US-10-017-161-1299	Sequence 1299, App
18	554.8	57.6	886	16	US-10-292-798-1067	Sequence 1067, App
19	470.2	48.8	943	15	US-10-023-597-57	Sequence 57, App1
20	456.8	47.4	952	15	US-10-023-597-59	Sequence 59, App1
21	452.6	47.0	951	15	US-10-023-601-89	Sequence 89, App1
22	445.6	46.3	953	15	US-10-023-597-63	Sequence 63, App1
23	443.8	46.1	487	9	US-09-747-155-366	Sequence 366, App
24	443.6	46.1	942	15	US-10-023-601-99	Sequence 99, App1
25	443	46.0	978	15	US-10-023-601-91	Sequence 91, App1
26	436.8	45.4	934	16	US-10-024-212-21	Sequence 21, App1
27	436.8	45.4	1330	15	US-10-017-161-323	Sequence 323, App
28	436.8	45.4	1330	15	US-10-292-798-289	Sequence 289, App
29	435.6	45.2	940	16	US-10-023-597-121	Sequence 121, App
30	435	45.2	930	9	US-09-886-055-22	Sequence 22, App1
31	435	45.2	930	10	US-09-804-291-22	Sequence 22, App1
32	435	45.2	930	13	US-10-343-650A-399	Sequence 399, App
33	434.4	45.1	961	15	US-10-023-597-91	Sequence 91, App1
34	429.8	44.6	934	15	US-10-023-597-125	Sequence 125, App
35	427.6	44.4	943	15	US-10-024-399-33	Sequence 33, App1
36	425.8	44.2	961	15	US-10-023-597-81	Sequence 81, App1
37	423.2	43.9	1342	15	US-10-017-161-315	Sequence 315, App
38	423.2	43.9	1342	16	US-10-292-798-281	Sequence 281, App
39	422.8	43.9	940	15	US-10-023-601-69	Sequence 69, App1
40	422	43.8	1336	15	US-10-017-161-811	Sequence 811, App
41	422	43.8	1336	16	US-10-292-798-697	Sequence 697, App
42	422	43.8	1341	17	US-10-467-252-92	Sequence 92, App1
43	421.6	43.8	1342	15	US-10-017-161-321	Sequence 321, App
44	421.6	43.8	1342	16	US-10-292-798-287	Sequence 287, App
45	421.4	43.8	915	16	US-10-387-629-71	Sequence 71, App1

ALIGNMENTS

RESULT 1
US-10-023-597-23
Sequence 23, Application US/10023597
Publication No. US20030109692A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: B1, Lt
APPLICANT: Ballinger, Robert A.
APPLICANT: Caeman, Stacey J.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Baumgartner, Jason C.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20030109692A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-224AD
CURRENT APPLICATION NUMBER: US/10/023, 597
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256, 635
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/259, 743
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/289, 327
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 60/261, 498
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/263, 689
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/267, 464
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/271, 021
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/275, 946
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/278, 150
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/285, 718
PRIOR FILING DATE: 2001-04-03

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 128
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23
 LENGTH: 963
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-023-597-23

Query Match 100.0%; Score 963; DB 15; Length 963;
 Best Local Similarity 100.0%; Pred. No. 2,5e-289;
 Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 421 GTTGTGCT 480
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QY 901 CTTGAGAGAACTTTTCCAGATTAAGTTTCTTGAAAAATTTAGAAACGAAAG 960
 DB 901 CTTGAGAGAACTTTTCCAGATTAAGTTTCTTGAAAAATTTAGAAACGAAAG 960
 QY 961 AGA 963
 DB 961 AGA 963

RESULT 2

US-10-017-161-1301
 Sequence 1301, Application US/1001761
 Publication No. US2003014368A1
 GENERAL INFORMATION:
 APPLICANT: SUMA, MAKIKO
 APPLICANT: ASAI, KIYOSHI
 APPLICANT: AKIYAMA, YUTAKA
 APPLICANT: ABURATANI, HIROYUKI
 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 08435/0152
 CURRENT APPLICATION NUMBER: US/10/017,161
 PRIOR FILING DATE: 2002-12-18
 PRIOR APPLICATION NUMBER: JP 2001/246789
 NUMBER OF SEQ ID NOS: 2430
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1301
 LENGTH: 931
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: source
 LOCATION: (1)..(931)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (201)..(731)
 US-10-017-161-1301

Query Match 78.4%; Score 755.4; DB 15; Length 931;
 Best Local Similarity 99.9%; Pred. No. 1.5e-224;
 Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 267 AGAATATTTCTCTTCAAGAGGATGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 326
 DB 61 AGAATATTTCTCTTCAAGAGGATGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 QY 327 TTTCTAGTCTCTTCACT 386
 DB 121 TTTCTAGTCTCTTCACT 180
 QY 387 CACTGTGTACAGATCACTACATGTCCTCCCAAGGCTGTCTCTCTCTCTCTCTCTCTCTCT 446
 DB 181 CACTGTGTACAGATCACTACATGTCCTCCCAAGGCTGTCTCTCTCTCTCTCTCTCTCTCT 240
 QY 447 ACGGATGGGGGTTTGGGCTGTGCTCAACAGAAATATAGTTTCTCACTTTT 506
 DB 241 ACGGATGGGGGTTTGGGCTGTGCTCAACAGAAATATAGTTTCTCACTTTT 300
 QY 507 GTGAGCAACACTGTGCAATCACTAATGTGTGACATCTCCCTCTTGAAGCTCTCT 566
 DB 301 GTGAGCAACACTGTGCAATCACTAATGTGTGACATCTCCCTCTTGAAGCTCTCT 360
 QY 567 GCAAGGCTCTTACATAATGTGTGCAATCTTATGTGTGACCGTTGGGCTTGGG 626
 DB 361 GCAAGGCTCTTACATAATGTGTGCAATCTTATGTGTGACCGTTGGGCTTGGG 420
 QY 627 TGGCATGTGTGGGCTTTTATCTCTATGTTTATCTCTTCAAGATCTCGGGGTA 686
 DB 421 TGGCATGTGTGGGCTTTTATCTCTATGTTTATCTCTTCAAGATCTCGGGGTA 480

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QY	722	TCTTACACATTAATGSACTTCTCTTTCTTTGGAGTCAGAGCTTTTAAAGTACCCGAAACC	787
QY <td>723</td> <td>TCCCATATATATGTAATCTCTTTCTTTGGTCTTGAGTCTTTCATATGTTCTCAAAACC</td> <td>788</td>	723	TCCCATATATATGTAATCTCTTTCTTTGGTCTTGAGTCTTTCATATGTTCTCAAAACC	788
Db <td>924</td> <td>TCCCATATATATGTAATCTCTTTCTTTGGTCTTGAGTCTTTCATATGTTCTCAAAACC</td> <td>983</td>	924	TCCCATATATATGTAATCTCTTTCTTTGGTCTTGAGTCTTTCATATGTTCTCAAAACC	983
QY <td>788</td> <td>CTTTCATATTTAACCCCTGGACAGGGGAAAGTGTCTCCCTGTTCTATACCACTGTGTG</td> <td>847</td>	788	CTTTCATATTTAACCCCTGGACAGGGGAAAGTGTCTCCCTGTTCTATACCACTGTGTG	847
Db <td>984</td> <td>CTTTCATCTCTGGCCCTCGACGAAGGAAAGTGTCTCCCTGTTCTATACCAATATATGTC</td> <td>1042</td>	984	CTTTCATCTCTGGCCCTCGACGAAGGAAAGTGTCTCCCTGTTCTATACCAATATATGTC	1042
QY <td>848</td> <td>CCCATGTTTAACCCATTATTTACAGCCTGAGGAATAAGATGTCAAACTTGCCCTGAAG</td> <td>907</td>	848	CCCATGTTTAACCCATTATTTACAGCCTGAGGAATAAGATGTCAAACTTGCCCTGAAG	907
Db <td>1044</td> <td>CCCGTGTAAACCCATTATTCATATGCTGGAGCAAGAGATGTCAAAAGTGTCCCTGAAG</td> <td>1102</td>	1044	CCCGTGTAAACCCATTATTCATATGCTGGAGCAAGAGATGTCAAAAGTGTCCCTGAAG	1102
QY <td>908</td> <td>AGAACCTTTCCAGATAAGCTTTCTTGAAGAAAAATTT</td> <td>946</td>	908	AGAACCTTTCCAGATAAGCTTTCTTGAAGAAAAATTT	946
Db <td>1104</td> <td>AGAACTTTGGCGAAGAAAAATCTTTCTTAAAGAAAGATT</td> <td>1142</td>	1104	AGAACTTTGGCGAAGAAAAATCTTTCTTAAAGAAAGATT	1142

RESULT 6
US-10-02

Sequence, Application US/10024399
Publication No. US20030100491A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Murailidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Colman, Steven D.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Ballinger, Robert A.
APPLICANT: Verneet, Corinne A.M.
APPLICANT: Li, Li
APPLICANT: Shenoy, Suresh G.
APPLICANT: Caseman, Stacie J.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-224AE
CURRENT APPLICATION NUMBER: US/10/024,399

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? CURRENT FILING DATE: 2001-12-18
? PRIOR APPLICATION NUMBER: 60/256,635
? PRIOR FILING DATE: 2000-12-18
? PRIOR APPLICATION NUMBER: 60/259,743
? PRIOR FILING DATE: 2001-01-04
? PRIOR APPLICATION NUMBER: 60/299,327
? PRIOR FILING DATE: 2001-06-19
? PRIOR APPLICATION NUMBER: 60/261,498
? PRIOR FILING DATE: 2001-01-12
? PRIOR APPLICATION NUMBER: 60/263,689
? PRIOR FILING DATE: 2001-01-24
? PRIOR APPLICATION NUMBER: 60/267,464
? PRIOR FILING DATE: 2001-02-08
? PRIOR APPLICATION NUMBER: 60/271,021
? PRIOR FILING DATE: 2001-02-22
? PRIOR APPLICATION NUMBER: 60/275,946
? PRIOR FILING DATE: 2001-03-14
? PRIOR APPLICATION NUMBER: 60/278,150
? PRIOR FILING DATE: 2001-03-23
? PRIOR APPLICATION NUMBER: 60/285,718
? PRIOR FILING DATE: 2001-04-23
? Remaining Prior Application data removed - See File Wrapper or PALM
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? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1
? LENGTH: 976
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-024-599-1

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Best Local Similarity	83.5%;	Pred. No. 4.7e-205;		
Matches 786; Conservative	0;	Mismatches 155;	Indels 0;	Gaps 0

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QY	121	GGGGAACCTGGGCTTATATATCTGTATAGGGCTCAACTCTGGCTGGCATATCCCATGTA	187
Db	127	GGGGAACCTGGGCTTATATACCTTATAGGGCTGAACCTCAACCTGCACACTCCCATGTA	194
QY	181	CTTTTTCCTTCAACTTGTCCCTCGTAGATTATTAAGTTTCTCTACAGACCATATTCCAA	244
Db	187	CTTCTTCTTTTAACTCTCTTTAATAGATTTCGTCTTCACACTACCATCTCCAA	246
QY	241	AATGCTGATGAGTTTGTCTCAAGGAAGAACTATTTCTCTCAAGGAGTATGAGCA	300
Db	247	AATGCTGATGAGTTTGTCTCAAGGAAGAACTATTTCTCTCAAGGAGTATGAGCTCA	306
QY	301	GTTCTTCTTCTCTGTTTCTTGTCTTGTCTTGTAGTCTTCAATCCTGTCCGAGATGTGA	366
Db	307	GCCTCTTCTTCTGCTCTTGTGTGCTGTAGTCTTCACTCTGTACAGGATGGGTA	368
QY	361	GGACCGGTAGGGGGATCTGTAAACCACTGTGTACAGATACCAATGCTCTCCCAAGT	422
Db	367	TGACCGGTAGGGGCATCTGTAAACCACTGTGTACAGATACCAATGCTCTTCCAGT	428
QY	421	GTTGTTCCTCTTTTACGTGGTGTCTACGGAGTGGGGTTTTGGGGCTGTGGCTATAC	486
Db	427	GTTGTTCCTCTTTTGTGGTGGCTATGGAGTGGGGTTTGTGGGGCTATGGGCCAAC	488
QY	481	AGGAATATATGATTTCTTCACTTGTGTGACACAACTGTGCATCTCATATGTGTA	546
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QY	541	CATCTTCCCTTCTTGAAGTCTCTGTCAACGGCTTTACATAAATGTCTGTGATTT	606
Db	547	CATCTTCTCTCTCTTGAAGTCTCTGTCAACGGCTTTACATGAATGAGTGTGATTT	608
QY	601	TATGTGTATACCGTTGAGCATTGGGGTGCCATTTTCCGTTTATCTTATATGTTT	666
Db	607	TATGTGTATGCTGTGATGAGTGAATGCCATGTCACTGTCTTATTTCTTATGCCCT	668
QY	661	TATTTCTTCCAGATTTCTCGCGTTATGTTCGTCTAGGGCAGGTCTAAAGCTTCAGTATG	722
Db	667	CATCTCTCTCAGATTTCTACAAACAGTTCTACAAAGCCAGGTCCAAAGCTTTAGTAC	728
QY	721	CTGAGCTCTCATATATATGAGTTTCTCTTTCTTGGGTCAGAGCTTTTACGTACT	786
Db	727	TTCAGTTCCCATATATATGATTTCTCTTTCTTGGTCTGGTGTCTTCATGTAATCT	788
QY	781	CAAAACCCCTTCATTTTACCTCTGACACAGGGGAAATGTCTCCCGTCTATACAC	844
Db	787	CAAAACCCCTTTCATCTCTGCTGCTCGAGGAAAGGATGTCTCTCTGTCTATACAT	846
QY	841	TGTGTGCCCCATGTTTAACCATTTATCTACAGCTGTAGAGATATGATGTAACCTGC	900
Db	847	AATGTGCCCCGTATAACCATTTATCTATAGCTGTGAGAAACAAGATGTCAAAAGTGC	906
QY	901	CTGAGAGAGAACCTTTTCAGAAATAGCTTTCTTGAATA	944
Db	907	CTGAGAGAGAACCTTTTGGCAAAATCTTTTCTTAAATA	946

RESULT 7
US-10-00

Sequence 13, Application US/10005041A
Publication No. US20030232331A1

; GENERAL INFORMATION:
 ; APPLICANT: Casman, Stacie J
 ; APPLICANT: Padigar, Muralidharan
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Shinkets, Richard A
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Gilbert, Jennifer A
 ; APPLICANT: Mayotte, Jane E

Qy	6	GGCGAAATCCTCCCTCCGTGACAGAGTTATTCCTCCAGAGTTATTCACACAGCGGGA	67
Dp	19	GCAGCCAAATAATCTCTGTGACAGAGTTATCCTGAAAGCTTAACCAACAGCGGGA	78
Qy	68	CTCCAGAGTCCCGCTCTTCTTCTGTTTCTAGGTTTCTACCGGCTACGGTGTGGGAAAC	127
Dp	79	CTCGGGATCCCCCTCTTCTCTCTGTTCTGGGTTTCTACAGGGTCAACGTGGGGGAAC	138
Qy	128	CTGGGCTTGATATCTGATAGGGGTCACTCTCGCTGATATCCCAATGATCTTTC	187
Dp	139	CTGGGCTTGATATACCTGATTTGGGTGAACCTCACTGACACATCCCAATGATCTTTC	198
Qy	188	CCCTTAATCTGTCCTCTGTAGATTTTAGTTTCTCTAGACATCATTTCCAAATGCTG	247
Dp	199	CTTTTAACTCTCTTATATGATTTCTGTTTCCACTCACTCACTCCCAAAATGCTG	258
Qy	248	ATGAGTTTGTCTCAGAGAAACAATATTTCCCTCAGAGGAGTATGATAGTCTTC	307
Dp	259	ATGAGTTTGTCTCAGAGAAACAATATTTCCCTCAGAGGAGTATGATAGTCTTC	318
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Dp	319	TTCCTCTGTTCTTTTGTGTGTCTGTAGAGCTTCACTCTGTCAACAGTGTGATGACGC	378
Qy	368	TACGTGGGATGTATAACCACTGTGTATACATCACTCACTGCTCCAGGTGTGTG	427
Dp	379	TACGTGGGATGTATAACCACTGTGTATACATCACTCACTGCTCCAGGTGTGTG	438
Qy	428	CTTCCTTTTACGTGGGTCTACGGGATGGGGTTTTTGGGCTGTGCTATACAGGAAT	487
Dp	439	CTTCCTTTTGTGGGTCTACGGGATGGGGTTTTTGGGCTGTGCTATACAGGAAT	498
Qy	488	ATAGGTTTCTACCTTTTGTGACAGACAACTTGTCACTACATACATGTTGATACCTTT	547
Dp	499	ATAGGTTTCTACCTTTGTGTGTGTGACAACTTGTCACTATTTCAATGTGTGATACCTTT	558
Qy	548	CCCTTTCTTGAAGCTCTCTGCAAGGCTTTTACATAATGTCTGTGATCTTTTATGTT	607
Dp	559	CCCTCTCTTGAAGCTCTCTGCAAGGCTTTTACATAATGATAGCGGGTGTCTTTTATGTT	618

QY	8	GGCGAGACTCTCTCTCCGTACACAGAGTTATCTCTCCAGAGCTTAATCCACACAGCCGGG	67
Db	4	GCAGCCAAAATCTTTCTGTGACACAGATTATCTCGAAGGCTTAACCCACACGCCGGG	63
QY	68	CTCCAGAGTCCCCCTCTTCTGCTATTCTGATTTAGAGGGTCAACGGGAGGGGAAAC	127
Db	64	CTGGCGAATCCCCCTTTCTTCCGTTCGTGGATTTCACAGGTCACCGGGGGGAAAC	123
QY	128	CTGGGCTTGATPATTCGTGATAGGGCTCACTTCGCTGCATATCCCATGACTTTTTC	187
Db	124	CTGGGCTTGATPACCCTGATGGGCTGAACTCTCACTGCACCTCCCAATGATCTTCTTC	183
QY	188	CCCTTCAACTGTCCCTCGTAGATTATTTAGTTCTCTACGACCAATATCTCCCAAAATGCTG	247
Db	184	CTTTTAACTCTCTTATATGATTTTCGTTTCCCACTCACTCCCAAAATGCTG	243
QY	248	ATGAGCTTTGCTCAAGSAAAGAACATTAATTCCTCAAGSGTAGTGAAGTACTCTTC	307
Db	244	ATGAGCTTTTGTCTCAAGSAAAPATCATTTCTTCAAGGGGTATGACTCAAGCTCTTC	303
QY	308	TTCTTCTGTCTTGTGCTTTTCTTGAGTCTTCACTCTGTGGCGATGCTGAGAGCCGC	367

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Db      304 TTCTTGCTCTCTTTGCTGCTCTGAGTCTTATCTCTGACGCAATGCGCTATGACCCG 363
Qy      368 TAGGTGGGCACTGTGTAACCACTGTTGTACAGCATCAACATGTTCCCGAGTGTGTTG 427
Db      364 TAGGTGGGCACTGTGTAACCACTGTTGTACAGCATCAACATGTTCCCGAGTGTGTTG 423
Qy      428 CTCCTTTTACAGGAGTCTACAGGAGTGGGGGTTTGGGGCTGTGCTCATCAGAAAT 487
Db      424 CTCCTTTTGTGGGCTATGGAGTGGGTTTGTCTGGGCTCAGGCCACACAGGAGAC 483
Qy      488 ATAGTGTTCACCTTTTGTGACAGACACTTGTCACTACATATGTGTACATCTT 547
Db      484 ATATGAACTGACCTTCTGTGCTGACACACTTGTCACTATTCATATGTGTACATCTT 543
Qy      548 CCCCTTGTAGCTCTCTGCAAGGCTTCAATTAATGTCTGTGATCTTTATTTT 607
Db      544 CTCCTCTTGTAGCTCTCTGCAAGGCTTCAATTAATGTCTGTGATCTTTATTTG 603
Qy      608 GTGACCGTGTGCAATTTGGGGTGGCCCATTTGTGCGTTTATCTCTATAGTTTATCTT 667
Db      604 GTGCTGTGTAGCTGTGAAATGCCATTTGTCACTGTTTATTTCTATGCGCTCATCTC 663
Qy      668 TCCGACATTTCCCGGTTAGTTTGTCTGAGGAGGCTTAAAGCCTTCACTGAGTCCAGC 727
Db      664 TCCGACATTTCAACAAGTTTCAACAAGGAGGCTCAAAAGCCTTTAGTACTTGCAT 723
Qy      728 TCCACATTAATTGAGTTCCTTTCTTTTGGTCAAGAGCTTTTACGTACCTCAACCC 787
Db      724 TCCACATTAATTGAGTTCCTTTCTTTTGGTCTGAGCTTTTCAATGATCTCAAAACC 783
Qy      788 CTTTCCATTTTAAACCCCTGAGACCAAGGAAAGTGTCTCTCTGTTCTATACACTGTGGTG 847
Db      784 CTTTCCATTTTAAACCCCTGAGACCAAGGAAAGTGTCTCTCTGTTCTATACCAATAAGTC 843
Qy      848 CCCATGTTTAAACCATTAATCTACAGCCTGAGCATTAAGATGTCAACCTTGCCCTGAAG 907
Db      844 CCCGTTTAAACCATTAATCTATAGTGTGAGAAACAAGATGTCAAAAGTGTCCCTGAGG 903
Qy      908 AGAAGCTTTTCCAGATTAAGTTCCTTTGA 937
Db      904 AGAAGCTTTGCGCAGAAAAATCTTTCTTAA 933

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RESULT 9
US-09-804-291-50
; Sequence 50: Application US/09804291
; Publication No. US20030088059A1
; GENERAL INFORMATION:
; APPLICANT: ZOZULA, SERGEY
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME
; FILE REFERENCE: P 0279005
; CURRENT APPLICATION NUMBER: US/09/804,291
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 60/188,914
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/192,033
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/198,474
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/199,335
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: 60/207,702
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/213,849
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/226,534
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/230,732
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/266,862
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 529
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 50
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-291-50
Query Match      71.8%; Score 691.6; DB 10; Length 933;
Best Local Similarity 84.0%; Pred. No. 1,2e-204;
Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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Qy      8 GCCGAGAACTCTCTCTGCTGACAGATTAATCTTGTGACAGGCTTAATCCACCAAGCCGGA 67
Db      4 GCAGCCAAAACCTTCTGTGACAGATTAATCTTGTGAGGCTTAAACCAAGCCGGA 63
Qy      68 CTCAGGCTCCGCTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 127
Db      64 CTCAGGATCCCTCTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 123
Qy      128 CTGGGCTGTATTAATCTGTATAGGCTCAACTCTGCTGCTCATATCCCATGTACTTTTTC 187
Db      124 CTGGGCTGTATTAATCTGTATAGGCTCAACTCTGCTGCTCATATCCCATGTACTTTTTC 183
Qy      188 CCCCTCAACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 247
Db      184 CTTTTAACCTCTCTTAAATAGATTTCTGTTTCTCACTAATCACTCTCCAAATGCTG 243
Qy      248 ATGAGTTTGTCTCAAGAAACATTAATCTTCTTCAAGGCTATGAGTCACTTCTTC 307
Db      244 ATGAGTTTGTCTCAAGAAACATTAATCTTCTTCAAGGCTATGAGTCACTTCTTC 303
Qy      308 TTTCTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 367
Db      304 TTTCTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 363
Qy      368 TAGGTGGGCACTGTGTAACCACTGTTGTACAGCATCAACATGTTCCCGAGTGTGTTG 427
Db      364 TAGGTGGGCACTGTGTAACCACTGTTGTACAGCATCAACATGTTCCCGAGTGTGTTG 423
Qy      428 CTCCTTTTACAGGAGTCTACAGGAGTGGGGGTTTGGGGCTGTGCTCATCAGAAAT 487
Db      424 CTCCTTTTGTGGGCTATGGAGTGGGTTTGTCTGGGCTCAGGCCACACAGGAGAC 483
Qy      488 ATAGTGTTCACCTTTTGTGACAGACACTTGTCACTACATATGTGTACATCTT 547
Db      484 ATATGAACTGACCTTCTGTGCTGACACACTTGTCACTATTCATATGTGTACATCTT 543
Qy      548 CCCCTTGTAGCTCTCTGCAAGGCTTCAATTAATGTCTGTGATCTTTATTTT 607
Db      544 CTCCTCTTGTAGCTCTCTGCAAGGCTTCAATTAATGTCTGTGATCTTTATTTG 603
Qy      608 GTGACCGTGTGCAATTTGGGGTGGCCCATTTGTGCGTTTATCTCTATAGTTTATCTT 667
Db      604 GTGCTGTGTAGCTGTGAAATGCCATTTGTCACTGTTTATTTCTATGCGCTCATCTC 663
Qy      668 TCCGACATTTCCCGGTTAGTTTGTCTGAGGAGGCTTAAAGCCTTCACTGAGTCCAGC 727
Db      664 TCCGACATTTCAACAAGTTTCAACAAGGAGGCTCAAAAGCCTTTAGTACTTGCAT 723
Qy      728 TCCACATTAATTGAGTTCCTTTCTTTTGGTCAAGAGCTTTTACGTACCTCAACCC 787
Db      724 TCCACATTAATTGAGTTCCTTTCTTTTGGTCTGAGCTTTTCAATGATCTCAAAACC 783
Qy      788 CTTTCCATTTTAAACCCCTGAGACCAAGGAAAGTGTCTCTCTGTTCTATACATAAGTC 847
Db      784 CTTTCCATTTTAAACCCCTGAGACCAAGGAAAGTGTCTCTCTGTTCTATACATAAGTC 843
Qy      848 CCCATGTTTAAACCATTAATCTACAGCCTGAGCATTAAGATGTCAACCTTGCCCTGAAG 907
Db      844 CCCGTTTAAACCATTAATCTATAGTGTGAGAAACAAGATGTCAAAAGTGTCCCTGAGG 903
Qy      908 AGAAGCTTTTCCAGATTAAGTTCCTTTGA 937
Db      904 AGAAGCTTTGCGCAGAAAAATCTTTCTTAA 933

```

RESULT 10

US-10-343-650A-395
 ; Sequence 395, Application US/10343650A
 ; Publication No. US20040067499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HAGA, TATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 395
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(933)
 ; US-10-343-650A-395

Query Match 71.8%; Score 691.6; DB 13; Length 933;
 Best Local Similarity 84.0%; Pred. No. 1.2e-204;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

```

QY 8 GCCGAGAACTCCTCCGTCAGAGATTATCTCGAGGCTTATCCACAGCGGGA 67
DB 4 GCAGCCAAAACCTCTGTGACAGAGTTATCTCGAAGGTTAACCAACAGCGGGA 63
QY 68 CTCGAGGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB 64 CTCGAGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
QY 128 CTCGAGGTGATTAATCTGATAGGCTCACTCTCGCTGATATCCCATCTACTTTC 187
DB 124 CTCGAGGTGATTAATCTGATAGGCTCACTCTCGCTGATATCCCATCTACTTTC 183
QY 188 CCGCTCACTTGTCCCTGTAAGTTTAACTTCTCTGACACCATATCCCAAAATGCTG 247
DB 184 CTTTAACTCTCTTAAATGATTTCTGTTCTCCACTACCATCTCCCAAAATGCTG 243
QY 248 ATGAGTTTGTCTCAAGAAAGAAATATTATCTCTCAAGAGGTATGAGTCAGTTCTTC 307
DB 244 ATGAGTTTGTCTCAAGAAAGAAATATTATCTCTCAAGAGGTATGAGTCAGTTCTTC 303
QY 308 TTTCTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
DB 304 TTTCTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 363
QY 368 TAGGTGGGCACTGTATACCACTGTGTGACAGATCACCATGTCCTCCAGAGTGTGTTG 427
DB 364 TAGGTGGGCACTGTATACCACTGTGTGACAGATCACCATGTCCTCCAGAGTGTGTTG 423
QY 428 CTCCTTTTACTGGGTCTTAAGGATGGGGGTTTGGGGCTGTGGCTCAATACAGAAAT 487
DB 424 CTCCTTTTGTGGGTCTTAAGGATGGGGGTTTGGGGCTGTGGCTCAATACAGAAAT 483
QY 488 ATAGTTTCTCACTTTTGTGAGACAACTTGTCAATCACTACATGTGATGATCTT 547
DB 484 ATATAGAACCTGACCTTCTGTGTGACAACTTGTCAATCACTACATGTGATGATCTT 543
QY 548 CCGCTTCTGAGGTCTCTCTGCAAGGCTTCTCAATTAATGTCTGTGATCTTTATGTT 607
DB 544 CCGCTTCTGAGGTCTCTCTGCAAGGCTTCTCAATTAATGTCTGTGATCTTTATGTT 603
QY 608 GTACCGGTGGCACTTGGGGTGGCAATGTGTGCGTTTATCTCTTATGTTTATCTT 667

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★

RESULT 11

US-10-220-382-35
 ; Sequence 35, Application US/10220382
 ; Publication No. US2003011911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: LAU, Preethi
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: SHIH, Leo L.
 ; APPLICANT: TRIBOULEY, Catherine
 ; APPLICANT: LU, Dyrng, Aina M.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: KHAN, Farrah A.
 ; APPLICANT: POLICKY, Jennifer L.
 ; APPLICANT: AU-YOUNG, Janice
 ; APPLICANT: YANG, Junming
 ; APPLICANT: HARLAND, Lee
 ; APPLICANT: WALSH, Roderick T.
 ; APPLICANT: LO, Terence P.
 ; APPLICANT: BOROMSKI, Mark L.
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-0044 PCT
 ; CURRENT APPLICATION NUMBER: US/10/220,382
 ; PRIOR FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 35
 ; LENGTH: 933
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: incyte ID No. US2003011911A1 7472439CBI
 ; US-10-220-382-35

Query Match

Best Local Similarity 71.8%; Score 691.6; DB 15; Length 933;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY 8 GCCGAGAACTCCTCCGTCAGAGATTATCTCGAGGCTTATCCACAGCGGGA 67
DB 4 GCAGCCAAAACCTCTGTGACAGAGTTATCTCGAAGGTTAACCAACAGCGGGA 63
QY 68 CTCGAGGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
DB 64 CTCGAGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123

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Qy	128	CTGGCGCTGATAATCTCTGATTAAGGGCTCAAACTCTGGCTGACATATCCCAATGACTTTTC	187
Db	124	CTGGCGCTGATAATCCCTGATTAAGGGCTGAACTCTCACTGCACTCCCAATGACTTTTC	183
Qy	188	CCCTTCAACTGTGCTCTGATAGATTTTATGTTTCTGTACGACCAATCAATCCCAATATGCTG	247
Db	184	CTTTTAACTCTCTTATATAGATTTCTGTTTCTCACTACCAATCACTCCCAAAATGCTG	243
Qy	248	ATAGATTGTGCTCAAGGAAAGAACTTTATTTCTTCAAGGGTGTATAGAGTCACTTTC	307
Db	244	ATAGATTGTGCTCAAGGAAAGAACTTTCTTCTTCAAGGGTGTATATCTCACTCTTTC	303
Qy	308	TTCCTGTGTTCTTTGTCTTTTCTGAGTCTTCATCTGTGCGCGATGTGAGAGACGC	367
Db	304	TTCCTGTGTTCTTTGTCTTTCTCTAGTCTTCATCTGTGAGGATGTGCTATGACGCG	363
Qy	368	TAGTGGGCGATCTGTAAACCACTGTTGTATACAGATCACTATGTCCCAAGTGTGTTG	427
Db	364	TAGTGGCCATCTGTAAACCACTGTTGTATACAGATCACTATGTCTTGCAAGTGTGTTG	423
Qy	428	CTCTCTTTTACTGGGTGTCTACGGGATGTGGGGTTTGTGGGCGTGTGCTCATACGAAAT	487
Db	424	CTCTCTTTGTGGGTGCTCATATGGGATGTGGGGTTTGTGGGGCCATATGGCCACACGGAAGC	483
Qy	488	ATAGTGTGTTCTACCTTTTGTGTGACAAACCTGTGTCAATCACTCATATGTGTGACATCTT	547
Db	484	ATATATGACCTGACCTTCTGTGTGTACAAACCTGTGTCAATCAATTCATATGTGTGACATCTT	543
Qy	548	CCCCCTTCTTGAGCTCTCTGTGCAACGGCTTTACATAAATGTCTGTGTATCTTTATTTGTT	607
Db	544	CCCTCTCTTGAGCTCTCTGTGCAACAGCTTTACATGAATGTAGCTGTGGTCTTTATTTATGTTG	603
Qy	608	GTAACCGTTGGCAATTGAGGGGCCCAATGTGTGCGTTTATCTCTPATATGTTTATTTCTT	667
Db	604	GTAACCGTTGACCTTGGAAATGCCCAATGTGTGCACTGTCTTTATTTCTATGCCCCATCTCTC	663
Qy	668	TCCAGCAATCTCCGCGTTAGTTCTGTGTGAGGCGAGGTCCTAAAGCCTTCAGTAGTGTGAGC	727
Db	664	TCCAGCAATCTCACACAACAGTTCTACAGAAAGGCAAGTCCAAAGCCTTATAGTACTGTGAGT	723
Qy	728	TCCATACATAATGACATTTCTCTTTCTTTGAGTGTGAGAGCTTTATGATCTTCAAAACC	787
Db	724	TCCCATATATATGTATGTTCTCTTTCTTTGTTGTGTGCTTTTCAATGATCTTCAAAACC	783
Qy	788	CTTTCATTTTACCCCTGTGACAGAGGGAAATGTCTCCCTGTTTCTATACCATGTGTGTG	847
Db	784	CTTTCATCTCTGCCCTGTGACAGAGGAAATGTCTCCCTGTTTCTATACCATATATGTC	843
Qy	848	CCCATGTTTAAACCATTAATCTACAGCCTGTGAGGAATAGATGTCAAACTGTGCCCTGAG	907
Db	844	CCCGTGTATAACCACTTAATCTATACCTGTGAGGAACAAGATGTCAAAAGTGTGCCCTGAGG	903
Qy	908	AGAACTTTTTCAGAAATAAAGCTTTTCTTGA 937	
Db	904	AGAACTTTGGCAGAAAAATCTTTTCTTGA 933	

RESULT 12
US-10-017-161-749
Sequence 749, Application US/10017161
Publication No. US20030143668A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIHO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABRUTANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18

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1 NUMBER OF SEQ ID NOS: 2430
2
3 SOFTWARE: PatentIn Ver. 2.1
4
5 SEQ ID NO: 749
6
7 LENGTH: 1336
8
9 TYPE: DNA
10
11 ORGANISM: Homo sapiens
12
13 FEATURE:
14
15 NAME/KEY: source
16
17 LOCATION: (1)..(1336)
18
19 FEATURE:
20
21 NAME/KEY: CDS
22
23 LOCATION: (20)..(1136)
24
25 OS:10-017-161-749

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Query Match	68.3%;	Score 657.4;	DB 15;	Length 1336;
Best Local Similarity	80.2%;	Pred. No. 7.4e-194;		
Matches 772; conservative	0;	Mismatches 191;	Indels 0;	Gaps 0;

Qy	1	AATGGGTGGCGAAGAACTCTCTCCGAGACAGAGTTATCTCGACGGTTATCCACCA	60
Ds	200	AATGGCTGTGAAGATTCTCTTCGAGACAGTTATCTCGACGGTTATCCACCA	259
Qy	61	GCGGGACATCCAGGTCCCGGCTTTCTTCTGTCTAGGTTCTACGGATCAGGAGT	120
Ds	260	ACGGGAGATCCAGATCCCGCTTCTCTCTGTCTTAGGCTTCTAGTGTCACTGTGGT	319
Qy	121	GGGGAACCTGGGCTTGATATCGTATAGGGCTCACTCCGCTCATATCCCATGTA	180
Ds	320	GGGGAACCTGGGCTTGATATCCGTATAGGGCTCACTCTTGCACACCCCTTAGTA	379
Qy	181	CTTTTCCCGCTTCAACTGTGCCCTCGTAGATTYTAGTTCTCTACGACCATCATTTCCAA	240
Ds	380	CTTCTTCCCTATACCTGTCTCTCATAGATTCTCGTATTCAGAGTTATCATCTCCAA	439
Qy	241	AATGCTGAATGATTTGTGCTCAAGAAAGACATTAATCTCTCAGGGGTGATAGTCA	300
Ds	440	AATGCTGAATGATTTGTCTTAAGAAAGACATCTCTACGAGGATGATATATCTCA	499
Qy	301	GTTCTCTTCTTCTGTTTCTTTGTCTTTTCTTGAGTCCCTCATCTGTGCGGATGATGA	360
Ds	500	GCTCTCTTCTTCTTCTTCTTTGTGTCTGTGAGTCCCTCATCTGTGACATAGGCGTA	559
Qy	361	GGACGGCTACGGGGGACATCTATACCAACAGTTGTACAGATACCATATCTCCCGAGT	420
Ds	560	TGACCGCTATGGGCACTGTATACCACTGTTGTATATGTATACCATGTCTCCCGAGT	619
Qy	421	GTTGTTGCTCTTTTACTGGGTTGTCACGGATGGGGGTTTGTGGGCTGTGACTCATAC	480
Ds	620	GTTGTTTCTCTTTTGTGGGTTGTCATAGGAATGGGGTTTGTGGGGCCATGAGCCACAC	679
Qy	481	AGGAATATAGAGTTTCTCACCTTTTGTAGACAGCAACTGTCAATCATATCATGTGTGA	540
Ds	680	AGCGTGCATGATGGGTGTGACCTTCTGTGCATTAACCTTGTATACCATATCATGTGTGA	739
Qy	541	CATCTTCCCGCTTCTTGAAGCTCTCTCGAACAGGCTTTATACAAATATGCTGTGATCTT	600
Ds	740	CATCTTCCCGCTTCTTGAAGTGTGCTTACACAGACCTATGTAAATGACTGTGATGTT	799
Qy	601	TATGTTGTGACCGTTGTGCAATTGGAGGAGCCATTGTGCGGTTTATGCTTATAGTTT	660
Ds	800	TGTTGTTGGGCAATGTATTTGTGTGTGCCCAAGTACCATTTATTTCTCTATGTCT	859
Qy	661	TATCTTTTCAGCAATTCGCGGTTAGTTGTGCTGAGGAGGCTTAAAGCTTCATAGTA	720
Ds	860	CATTCCTCTACACATCTTCCACATGTATTCACAGGAGGAGCTCCAAAGCCTTCAGAC	919
Qy	721	CTGACACTCTCATATATGAGTTTGCTTTCTTTGGGTACAGAGCTTTACAGTACT	780
Ds	920	CTGACACTCTCATATATGAGTTTCTCTCTTTCTTTGGGTACAGAGCATTCATGACTCT	979
Qy	781	CAAAACCCCTTCATTTTAAACCCCTGACACAGGGAAGATGCTCTCCCTGTTCTATACAC	840
Ds	980	CAAAACCCCTTCTTTTAAAGCTATGAACAGGGAGAGGTCTTCTCCATTTCTATACAC	1039

QY 841 TGTGTGTCCTCATTTTAAACCATTTATCTACACCTGAGGATAGGATGTCAAACTTGC 900
 DB 1040 TGTGTGTCCTCATTTTAAACCATTTATCTACACCTGAGGATAGGATGTCAAACTTGC 1099
 QY 901 CCTGAAGAGAACTTTTCCAGAAATAGCTTTCTGTAATAAATTTTAAAGACAGAAAG 960
 DB 1100 TCTAAAGAAATCTTGAACAAATATGATTTCTCTAGAAAAGGGCAATGCTCAGAAAG 1159
 QY 961 AGA 963
 DB 1160 AAA 1162

RESULT 13

US-10-292-798-653
 ; Sequence 653, Application US/10292798
 ; Publication No. US20030235833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUMA, MAKIKO
 ; APPLICANT: ASAI, KIYOSHI
 ; APPLICANT: AKIYAMA, YUTAKA
 ; APPLICANT: AUBURATANI, HIROYUKI
 ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: 084335/166
 ; CURRENT APPLICATION NUMBER: US/10/292,798
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 10/017,161
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2001-246789
 ; PRIOR FILING DATE: 2001-06-18
 ; NUMBER OF SEQ ID NOS: 2070
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 653
 ; LENGTH: 1336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; LOCATION: source
 ; FEATURE: (1)..(1336)
 ; NAME/KEY: CDS
 ; LOCATION: (201)..(1136)
 ; US-10-292-798-653

Query Match 68.3%; Score 657.4; DB 16; Length 1336;
 Best Local Similarity 80.2%; Pred. No. 7.4e-194;
 Matches 772; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

QY 1 AATGCTGCCGAGAACTCTCTCCCTGACAGAGTTTATCTCGCAGCCTTATCCACCA 60
 DB 200 AATGCTGCCGAGAACTCTCTCCCTGACAGAGTTTATCTCGCAGCCTTATCCACCA 259
 QY 61 GCCGGAGCTCCAGAGTCCCGCTTCTCTGTTTCTAGGTTCTACGGGCTCAGGGTGT 120
 DB 260 ACCGGAGCTCCAGATCCCGCTTCTCTGTTTCTAGGTTCTACGGGCTCAGGGTGT 319
 QY 121 GGGGAACCTGGCTTGAATCTGTATAGGCTCAACTCTGCGCTGCATATCCCATGTA 180
 DB 320 GGGGAACCTGGCTTGAATCTGTATAGGCTCAACTCTGCGCTGCATATCCCATGTA 379
 QY 181 CTTTTCCTCCCTCAACTGCTGCTGCTAGATTTTATTTCTCTACAGCAATCATTCCTCA 240
 DB 380 CTTTTCCTCCCTCAACTGCTGCTGCTAGATTTTATTTCTCTACAGCAATCATTCCTCA 439
 QY 241 AATGCTGATGATTTTGTCTCAAGAGAACTATTTCTTCAAGGGTGTATGATGTA 300
 DB 440 AATGCTGATGATTTTGTCTCAAGAGAACTATTTCTTCAAGGGTGTATGATGTA 499
 QY 301 GTTCT 360
 DB 500 GCT 559

QY 361 GGAACCCCTACGTCGGCATCTGTAAACCATCTGTTGATACATCAATCTCTCCCAAGT 420
 DB 560 TGACCCCTATGTCGGCATCTGTAAACCATCTGTTGATACATCAATCTCTCCCAAGT 619
 QY 421 GGTGTGTCCTCTTACTGAGGCTGTACAGGATGGGAGTTTGTGGGCTGTGCTCATAC 480
 DB 620 GTGTGTTCTCTCTTGTGAGGCTGTATAGGATGGGAGTTTGTGGGCTGTGCTCATAC 579
 QY 481 AGGAATATAGTGTTCACCTTTTGTGACACACCTTGTCAATCATCATATGTGTGA 540
 DB 680 AGGTGATGATGGGTGTGACCTTCTGTGCAATPACCTTGTCAACCATCATATGTGTGA 739
 QY 541 CATCTTCCCTCTTGTAGCTCTCTGCAAGGCTCTTACATAATGCTGTGATCTT 600
 DB 740 CATCTTCCCTCTTGTAGCTGTGCTGTGACACAGACCATATGTGATGATGTGTG 739
 QY 601 TATTGTTGTACCGTTGGCATTTGGGTGCCATTTGTCGGTTTATCTCTTATGTTT 660
 DB 800 TATTGTTGTGGCATTTGATTTGGGTGCCACATCTTCAATTTCTATGTTCT 859
 QY 661 TATTCTTTCAGCATTTCCGGTGTAGTTCTGTGAGGAGGAGTCTAAAGCTTCAATAG 720
 DB 860 CATCTCTCAGCATCTTCCACATTTGATTCACAGGAGGAGTCCAAAGCTTTCAGCAC 919
 QY 721 CTGACGCTCTACATTAATTTGCAATTTCTTTCTTTTGGGTGAGGACTTTTACATCT 780
 DB 920 CTGACGCTCTCACAATTAATTTGCAATTTCTTTCTTTTGGGTGAGGACTTTTACATCT 979
 QY 781 CAAACCCCTTCATTTTACCCCTGAGCAGAGGAGAAAGTCTCCCTGTTCTATACAC 840
 DB 980 CAAACCCCTTTCTCTTTAGTATGACACAGGAGAGTCTCCCTATTTCTATACAC 1039
 QY 841 TGTGTGTCCTCATTTTAAACCATTTATCTACAGCTGAGGAATAGGATGTCAAACTTGC 900
 DB 1040 TGTGTGTCCTCATTTTAAACCATTTATCTACAGCTGAGGAATAGGATGTCAAACTTGC 1099
 QY 901 CCTGAAGAGAACTTTTCCAGAAATAGCTTTCTGTAATAAATTTTAAAGACAGAAAG 960
 DB 1100 TCTAAAGAAATCTTGAACAAATATGATTTCTCTAGAAAAGGGCAATGCTCAGAAAG 1159
 QY 961 AGA 963
 DB 1160 AAA 1162

RESULT 14

US-10-343-650A-397
 ; Sequence 397, Application US/10343650A
 ; Publication No. US20040067499A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGA, YATSUYA
 ; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: 31671-186347
 ; CURRENT APPLICATION NUMBER: US/10/343,650A
 ; CURRENT FILING DATE: 2003-07-21
 ; PRIOR APPLICATION NUMBER: JP 2000/237818
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: JP 2001/34434
 ; PRIOR FILING DATE: 2001-02-13
 ; NUMBER OF SEQ ID NOS: 694
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 397
 ; LENGTH: 942
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(942)
 ; US-10-343-650A-397

Query Match 67.6%; Score 650.6; DB 13; Length 942;
 Best Local Similarity 80.9%; Pred. No. 7.6e-192;

Matches 758; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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QY 1 AATGGCTGGCGAAGTCTCTCCCTGACAGAGTTATCTCGCAGGCTTAAATCCACA 60
Db 6 AATGGCTGGCGAAGTCTCTCCCTGACAGAGTTATCTCGCAGGCTTAAATCCACA 65
QY 61 GCCGGAGCTCAGAGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 66 ACCGGAGCTCAGAGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
QY 121 GGGGAACCTGGGCTTGAATCTCTGATAGGGCTCACTCTCGCTGCAATATCCCATGTA 180
Db 126 GGGGAACCTGGGCTTGAATCTCTGATAGGGCTCACTCTCGCTGCAATATCCCATGTA 185
QY 181 CTTTTCCTCCCTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 186 CTTTTCCTCCCTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245
QY 241 AATGCTATGAGTTTGTCTCAAGAGAAATATTTCTTCTACAGGCTGATAGTCA 300
Db 246 AATGCTATGAGTTTGTCTCAAGAGAAATATTTCTTCTACAGGCTGATAGTCA 305
QY 301 GTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 306 GTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 365
QY 361 GGAGCGCTAGCGGAGCTCTGTAAACCACTGTGTACAGATCACATGTTCCCAAGT 420
Db 366 TGACCGGTATGTGGCCATCTGTAAACCACTGTGTACAGATCACATGTTCCCAAGT 425
QY 421 GTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 426 GTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 485
QY 481 AGGAATATAGTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
Db 486 AGCGTGATATAGTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545
QY 541 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 546 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 605
QY 601 TATGTTGTGACGCTTGGCATGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 606 TATGTTGTGACGCTTGGCATGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 665
QY 661 TATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 666 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 725
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Db 726 CTGAGCTCTCAATATGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 785
QY 781 CAAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 786 CAAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 845
QY 841 TGTGTGCTCCAGTGTAAACCAATTAATCAAGCTGAGGAATAGAGTGTCAAACTGC 900
Db 846 TGTGTGCTCCAGTGTAAACCAATTAATCAAGCTGAGGAATAGAGTGTCAAACTGC 905
QY 901 CCGAAGAGAACCTTTTCCAGAAATAGCTTTCTGTA 937
Db 906 TCTTAAAGAAATCTTGAACAAAATGATTTCTCTGA 942

```

APPLICANT: Velthen, Alex
 TITLE OF INVENTION: Olfactory and Pheromones G-Protein coupled Receptors
 FILE REFERENCE: 9409/2192
 CURRENT APPLICATION NUMBER: US/10/387,629
 NUMBER OF SEQ ID NOS: 254
 CURRENT FILING DATE: 2003-03-13
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 47
 LENGTH: 951
 TYPE: DNA
 ORGANISM: Homo Sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(948)
 OTHER INFORMATION:
 US-10-387-629-47

Query Match 67.6%; Score 650.6; DB 16; Length 951;
 Best Local Similarity 80.3%; Pred. No. 7,9e-192;
 Matches 758; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

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QY 1 AATGGCTGGCGAAGTCTCTCCCTGACAGAGTTATCTCGCAGGCTTAAATCCACA 60
Db 15 AATGGCTGGCGAAGTCTCTCCCTGACAGAGTTATCTCGCAGGCTTAAATCCACA 74
QY 61 GCCGGAGCTCAGAGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 75 ACCGGAGCTCAGAGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 134
QY 121 GGGGAACCTGGGCTTGAATCTCTGATAGGGCTCACTCTCGCTGCAATATCCCATGTA 180
Db 135 GGGGAACCTGGGCTTGAATCTCTGATAGGGCTCACTCTCGCTGCAATATCCCATGTA 194
QY 181 CTTTTCCTCCCTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 195 CTTTTCCTCCCTCAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 254
QY 241 AATGCTATGAGTTTGTCTCAAGAGAAATATTTCTTCTACAGGCTGATAGTCA 300
Db 255 AATGCTATGAGTTTGTCTCAAGAGAAATATTTCTTCTACAGGCTGATAGTCA 314
QY 301 GTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Db 315 GTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 374
QY 361 GGAGCGCTAGCGGAGCTCTGTAAACCACTGTGTACAGATCACATGTTCCCAAGT 420
Db 375 TGACCGGTATGTGGCCATCTGTAAACCACTGTGTACAGATCACATGTTCCCAAGT 434
QY 421 GTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db 435 GTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 494
QY 481 AGGAATATAGTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
Db 495 AGCGTGATATAGTGTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 554
QY 541 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 555 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 614
QY 601 TATGTTGTGACGCTTGGCATGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 615 TATGTTGTGACGCTTGGCATGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 674
QY 661 TATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 675 CATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 734
QY 721 CTGAGCTCTCAATATGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db 735 CTGAGCTCTCAATATGCAATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 794

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QY 781 CAACCCCTTCATTTTACCCCTGAGACGAGGGAAGTGTCTTCTATATACAC 840
Db 795 CAACCCCTTTCTCTTTTACCTAATGACGAGGCAAGTGTCTTCTATATACAC 854
QY 841 TGTGTGCCCCATGTTTAACTTAATCTACAGCCTGAGGAATAAGATGCAACTTGC 900
Db 855 TGTGTGCCCCATGCTCAACCCATTAATTATAGCCTGAGGAATAAGACGTCAAGTTGC 914
QY 901 CCTGAGAGAGACCTTTCCAGATAAGCTTTCTTGA 937
Db 915 TCTAAGAAAAATCTTGACAAAATGCAATTCTCTGA 951

Search completed: September 30, 2004, 06:05:29
Job time : 2255 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2004, 20:11:39 ; Search time 472 seconds
(without alignments)

8667.404 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 aatgctgcgcagagactcct.....ttttagaacaagaaagaga 963

Scoring table: IDENTITY NUC
Gapop 10-0, Gapext 1-0

Searched: 3373863 seqs, 2124099641 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N Geneseq 29Jan04:*

1: Geneseqn1980s:*\n2: Geneseqn1990s:*\n3: Geneseqn2000s:*\n4: Geneseqn2001as:*\n5: Geneseqn2001bs:*\n6: Geneseqn2002s:*\n7: Geneseqn2003as:*\n8: Geneseqn2003bs:*\n9: Geneseqn2003cs:*\n10: Geneseqn2004s:*

Pred. NO. is the number of results predicted by chance a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	963	100.0	963	6	AAFB8413	AaFB8413 Human GPC
2	960.4	99.7	994	4	AAH31675	Aah31675 Human Olf
3	937	97.3	960	9	ADD12748	Add12748 CDNA enco
4	755.4	78.4	931	9	ADC86616	Adc86616 Human GPC
5	751	78.0	935	4	AAH31668	Aah31668 Human Olf
6	694.2	72.1	991	6	ABS58782	Ab58782 Human G-P
7	694.2	72.1	1333	9	ADC85838	Adc85838 Human GPC
8	693	72.0	976	6	ABK97207	Abk97207 Human G-P
9	693	72.0	976	9	ADD60328	Add60328 Human G-P
10	692.4	71.9	953	6	ABT05655	Abt05655 GPCR 4 pr
11	691.6	71.8	933	5	AAH315910	AaH315910 DNA enco
12	691.6	71.8	933	5	AAH315910	AaH315910 DNA enco
13	691.6	71.8	933	5	AAH315910	AaH315910 DNA enco
14	691.6	71.8	933	5	AAH315910	AaH315910 DNA enco
15	691.6	71.8	933	5	AAH315910	AaH315910 DNA enco
16	690.2	71.7	930	4	AAH32421	Aah32421 Human Olf
17	687.4	68.3	989	4	ABS58834	Ab58834 Human G-P
18	657.4	68.3	1336	9	ADC86200	Adc86200 Human G-P
19	655.2	68.0	1655	6	AAH32449	Aah32449 Human G-P
20	650.6	67.6	942	6	ABZ43068	Abz43068 Human GPC
21	650.6	67.6	951	6	ABK68456	Abk68456 Human DNA
22	649.6	67.5	936	5	AAH315911	AaH315911 DNA enco
23	649.6	67.5	936	6	ABK40195	Abk40195 Human G-P

24	647.2	67.2	933	4	AAH32246	Aah32246 Human Olf
25	555	57.7	942	7	ABZ77877	Abz77877 Human G-P
26	554.8	57.6	886	9	ADC86614	Adc86614 Human GPC
27	480	49.8	984	4	AAH32275	Aah32275 Human Olf
28	477.4	49.6	937	6	ABS58757	Ab58757 Human G-P
29	477.4	49.6	937	6	ABS58759	Ab58759 Human G-P
30	477.4	49.6	937	6	ABS58758	Ab58758 Human G-P
31	472.6	49.1	984	4	AAH32381	Aah32381 Human Olf
32	472.6	48.6	937	6	ABS58756	Ab58756 Human G-P
33	460.6	47.8	943	9	ADD12782	Add12782 CDNA enco
34	460	47.8	943	9	ADD12784	Add12784 CDNA enco
35	458.2	47.8	942	6	AAH88430	Aah88430 Human GPC
36	456.8	47.4	952	6	AAH88431	Aah88431 Human GPC
37	454.8	47.2	945	7	ABZ77909	Abz77909 Human G-P
38	452.6	47.0	961	6	ABZ88087	Abz88087 Human GPC
39	445.6	46.3	953	6	AAH88433	Aah88433 Human GPC
40	443.8	46.1	487	4	AAH84039	Aah84039 Mouse Olf
41	443.6	46.1	942	6	ABO88092	Ab88092 Human GPC
42	443	46.0	978	6	ABZ88088	Abz88088 Human GPC
43	441.6	45.9	962	9	ADC79403	Adc79403 Human G-P
44	440.8	45.8	953	9	ADD12788	Add12788 CDNA enco
45	436.8	45.4	934	6	ABT04145	Abt04145 Human G-P

ALIGNMENTS

RESULT 1	AAFB8413	standard; CDNA; 963 BP.
XX	AAFB8413	
AC	AAFB8413	
XX	12-NOV-2002	(first entry)
DT	12-NOV-2002	(first entry)
XX	Human GPCR CDNA SEQ ID 23.	
DE	Human GPCR CDNA SEQ ID 23.	
XX	Human, anti-HIV; nootropic; antiaesthetic; antiarteriosclerotic; GPCR;	
KW	immunopressor; immunomodulator; cytoskeletal; antiinflammatory; AIDS;	
KW	antidiabetic; neuroprotective; anorectic; haemostatic; antibacterial;	
KW	fungicide; protozoal; virucide; human G-protein coupled receptor;	
KW	gene therapy; vaccine; cardiomyopathy; atherosclerosis; diabetes;	
KW	cell signal processing; cancer; obesity; neurodegenerative disorder;	
KW	cachexia; anorexia; Alzheimer's disease; Parkinson's disease;	
KW	immune disorder; graft versus host disease; bronchial asthma;	
KW	Crohn's disease; multiple sclerosis; haemophilia; infectious disease;	
KW	idiopathic thrombocytopenic purpura; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FN	WO200250275-A2.	
XX		
PD	27-JUN-2002.	
XX		
PR	18-DEC-2001; 2001WO-US048958.	
XX		
PR	18-DEC-2000; 2000US-0256635P.	
XX		
PR	21-DEC-2000; 2000US-0257876P.	
XX		
PR	04-JAN-2001; 2001US-0259743P.	
XX		
PR	10-JAN-2001; 2001US-0260718P.	
XX		
PR	12-JAN-2001; 2001US-0261498P.	
XX		
PR	24-JAN-2001; 2001US-0263689P.	
XX		
PR	08-FEB-2001; 2001US-0267464P.	
XX		
PR	22-FEB-2001; 2001US-0271021P.	
XX		
PR	14-MAR-2001; 2001US-0275946P.	
XX		
PR	23-MAR-2001; 2001US-0284591P.	
XX		
PR	18-APR-2001; 2001US-0285718P.	
XX		
PR	23-APR-2001; 2001US-0293277P.	
XX		
PR	19-JUN-2001; 2001US-0295327P.	
XX		
PR	16-AUG-2001; 2001US-0312902P.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		

This invention describes novel human G-protein-coupled receptor (GPCR) polypeptides which have anti-HIV, neurotropic, antitachypneic, procoagulant, antiarteriosclerotic, immunosuppressive, immunomodulator, cytoprotective, antiinflammatory, antidiabetic, neuroprotective, anorectic, haemostatic, antitubercular, fungicidal and virucidal activity. The products of the invention can be used in gene therapy or for vaccines. The GPCR polypeptide, GPCR nucleic acid and antibody are useful for treating, preventing or alleviating a GPCR-associated disorder or a pathological state in a subject e.g. cardiomyopathy, atherosclerosis, diabetes, or a disorder related to cell signal processing and metabolic pathway modulation. The GPCR polypeptide and nucleic acid are also useful for diagnosing the presence of or predisposition to a disease associated with altered levels of GPCR, particularly cancer. These polypeptides, nucleic acids and antibodies are also useful for treating or preventing obesity, neurodegenerative disorders, AIDS, cancer-associated cachexia, anorexia, Alzheimer's disease, Parkinson's disease, immune disorders, graft versus host disease, bronchial asthma, Crohn's disease, multiple sclerosis, haemophilia, idiopathic thrombocytopenic purpura or infectious disease. They can also be used to screen for potential agonist and antagonist compounds. The polypeptides are also useful as immunogens to produce antibodies or as vaccines. Anti-GPCR antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure such as in determining the efficacy of a given treatment regimen. The host cells are useful in producing non-human transgenic animals which are useful for studying the function and/or activity of GPCR protein and for identifying and/or evaluating modulators of GPCR protein activity. AAB84402-AAB84465 encode the human GPCR proteins represented in AAB71163-AAB71226

QY	AAAGSGCGCCGAAACATCCCTCCCGTGAACAAGTTTATCCCTCCGAGGCTTAATCCACA	60
Db	1 AATGCTGCCGAAATCTCTCTCCGTGACAAAGTTTATCCCTCCGAGGCTTAATCCACA	60
QY	61 GCCGGAACTCCAGTCCCGCTCTTCTCTGTTCTAGATTCTACGGGTCAAGTGT	120
Db	61 GCCGGAACTCCAGTCCCGCTCTTCTCTGTTCTAGATTCTACGGGTCAAGTGT	120
QY	121 GGGGAACCTGGGCTTATATCTGATAGGGTCAACTCCGCTGATATCCCAAGTA	180
Db	121 GGGGAACCTGGGCTTATATCTGATAGGGTCAACTCCGCTGATATCCCAAGTA	180
QY	181 GTTTTCCCTCAACTTCCCTCGTAGATTATGTTCTCTACGACCAATATCCCA	240
Db	181 GTTTTCCCTCAACTTCCCTCGTAGATTATGTTCTCTACGACCAATATCCCA	240
QY	241 AATGCTGATGATTTTGTCTCAAGGAAGAACTTATTTCTTCCACAGGGTATAGTCA	300
Db	241 AATGCTGATGATTTTGTCTCAAGGAAGAACTTATTTCTTCCACAGGGTATAGTCA	300
QY	301 GTTCTTCTTCTGTTCTTTGTCTTTTCTAGTCCCTTACTCCGTGCGGATGAGCA	360
Db	301 GTTCTTCTTCTGTTCTTTGTCTTTTCTAGTCCCTTACTCCGTGCGGATGAGCA	360
QY	361 GAGCCGCTACGTGGGATCTGTAAACCACTGTTTACAGATCAACATGTCTCCCAAGT	420

Db	361	GGACCGCTACGTGGGCGCATCTGTAAACCACTGTTGTACACATCAACAACTGTCCTCCCAAGGT	480
QY	421	GTGTTTGCCCTCTTTTCTCTGGGTGTCTACGGGATGGGGGCTTTTGGGGCTGTGGCTCTAC	480
Db	421	GTGTTTGCTCTTTTACTGGAGTGTCTACGGAGTGGGGGCTTTTGGGGCTGTGGCTCTAC	480
QY	481	AGGAATAATATAGTGTTCCTCACCTTTTGTGTGACACACACCTTGTCATCACTACATATGTGTGA	540
Db	481	AGGAATAATATAGTGTTCCTCACCTTTTGTGTGACACACACCTTGTCATCACTACATATGTGTGA	540
QY	541	CATCCTTCCCTCTCTGAGCTCTCGTGGACAGGGGCTTACATAATAGTCCGTGATCTT	600
Db	541	CATCCTTCCCTCTCTGAGCTCTCGTGGACAGGGCTTACATAATAGTCTGGTCACTTT	600
QY	601	TATGTTGTGACCGGTGGGCGATTGGGGGTGCCCATTTGTGCGCTTTTATCTCTATAGCTTT	660
Db	601	TATGTTGTGACCGGTGGGCGATTGGGGGTGCCCATTTGTGCGCTTTTATCTCTATAGCTTT	660
QY	661	TATCTCTTCACAGATCTCTCGGCTAGTTCGTGTGAGGGGAGGCTCTAAAGCCTCAAGTAG	720
Db	661	TATCTCTTCACAGATCTCTCGGCTAGTTCGTGTGAGGGGAGGCTCTAAAGCCTTCAAGTAG	720
QY	721	CTGACGCTCTCATATATGTACAGTTTCTCTTTCTTTGGGTCAAGACCTTTTACGTACT	780
Db	721	CTGACGCTCTCATATATGTACAGTTTCTCTTTCTTTGGGTCAAGACCTTTTACGTACT	780
QY	781	CAAAACCCCTTCATCTTACCCCTGGACAGAGGGGAAATGTCTCCCTGTCTATAACAC	840
Db	781	CAAAACCCCTTCATCTTACCCCTGGACAGAGGGGAAATGTCTCCCTGTCTATAACAC	840
QY	841	TGTGTGTGCCCATGTTTAAACCCATTATCTACAGCTGAGGAATATAGATGTCAAATTGC	900
Db	841	TGTGTGTGCCCATGTTTAAACCCATTATATCTAACAGCTGAGGAATATAGATGTCAAATTGC	900
QY	901	CTGAGAGAGAACCTTTCTCAGAAATATAGCTTTTCTGTGAAAATAATTTTATAGAAACGAAAG	960
Db	901	CTGAGAGAGAACCTTTCTCAGAAATATAGCTTTTCTGTGAAAATAATTTTATAGAAACGAAAG	960
QY	961	AGA 963	
Db	961	AGA 963	

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RESULT 2
ID AAH31675
AAH31675 standard; DNA; 994 BP.
AC
XX AAH31675;
XX
XX 30-JUL-2001 (first entry)
XX
XX Human olfactory receptor polynucleotide, SEQ ID NO: 248.
DE
XX
XX Human; olfactory receptor; OR; primary scent determination;
KM secondary scent determination; polypeptide library; odour receptor
KM scent profile; scent fingerprint; scent representation; ds.
KM
XX
XX Homo sapiens.
OS
XX
XX WO200127158-A2.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US027592.
XX
XX 08-OCT-1999; 99US-0158615P.
XX
XX 24-FEB-2000; 2000US-0184809P.
XX
XX (DIGI-) DIGISCENTS.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX

```

DR MPI: 2001-290713/30.
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 XX
 XX
 PS Claim 8; Page 276; 1857bp; English.

CC The present sequence is one of a number of isolated polynucleotides which
 CC encode polypeptides involved in olfactory sensation. The polynucleotides
 CC can be used in screening for olfactory agonists and antagonists. The
 CC methods allow for the determination of primary scents and the
 CC identification of the odor receptors used to detect these primary
 CC scents. The methods also enable determination of secondary scents and the
 CC identification of combinations of odor receptors that are involved in
 CC detecting such secondary scents. This enables the construction of a scent
 CC representation (also called a scent fingerprint or scent profile), which
 CC may be used to re-create and edit scents. Libraries of olfactory
 CC receptors are useful for determining the interaction pattern of a
 CC composition with the receptors, and can be used for determining
 CC differences in the olfactory faculties of different individuals
 XX
 XX

Sequence 994 BP; 201 A; 250 C; 207 G; 336 T; 0 U; 0 Other;

Query Match 99.7%; Score 960.4; DB 4; Length 994;
 Best Local Similarity 99.9%; Pred. No. 5.9e-265;
 Matches 961; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATGGCTGCGAGAACTCCTCCTCCGAGAGATTATCCTCGAGGCTTATCCACGAG 61
 DB 1 ATGGCTGCGAGAACTCCTCCTCCGAGAGATTATCCTCGAGGCTTATCCACGAG 60
 QY 62 CCGGAGCTCCAGAGTCCCGCTTCTCCTGTTTACGTTTACAGGGGTCAGGGTGG 121
 DB 61 CCGGAGCTCCAGAGTCCCGCTTCTCCTGTTTACGTTTACAGGGGTCAGGGTGG 120
 QY 122 GGGAACTCGGCTTGAATATCCTGATAGGGCTCAACTCTGCTGATATCCCATGAC 181
 DB 121 GGGAACTCGGCTTGAATATCCTGATAGGGCTCAACTCTGCTGATATCCCATGAC 180
 QY 182 TTTTCCCGCTCACTGCTGCTGCTGATATTTAGTTTCTCTCGACCAATCCCAAA 241
 DB 181 TTTTCCCGCTCACTGCTGCTGCTGATATTTAGTTTCTCTCGACCAATCCCAAA 240
 QY 242 ATGCTGATGATTTTGTCTCAGAGAGAACTTATTCCTTCAAGGGTGTATGACTGAG 301
 DB 241 ATGCTGATGATTTTGTCTCAGAGAGAACTTATTCCTTCAAGGGTGTATGACTGAG 300
 QY 302 TTTCTCTCTCTGTTTCTTCTTCTTCTGAGTCCCTTCACTGCTGCGGAGTGGAG 361
 DB 301 TTTCTCTCTCTGTTTCTTCTTCTTCTGAGTCCCTTCACTGCTGCGGAGTGGAG 360
 QY 362 GACCGCTACGTGGGATCTGTAACTGATGTTGATACAGATCAACATGCTCCCAAGTG 421
 DB 361 GACCGCTACGTGGGATCTGTAACTGATGTTGATACAGATCAACATGCTCCCAAGTG 420
 QY 422 TGTGTTGCTCTTTTACTGAGGTGTCTAGGGATGGGGGTTTTGGGGTGTGGTCTATAA 481
 DB 421 TGTGTTGCTCTTTTACTGAGGTGTCTAGGGATGGGGGTTTTGGGGTGTGGTCTATAA 480
 QY 482 GGAATAATAGTGTCTTCTACCTTTTGTGACAGAACCTTGATCACTACATGATGTGAC 541
 DB 481 GGAATAATAGTGTCTTCTACCTTTTGTGACAGAACCTTGATCACTACATGATGTGAC 540
 QY 542 ATCTTCCCTCTTCTGAGCTCTCTGCAAGGCTTCACTAATGATGCTGATCTTT 601
 DB 541 ATCTTCCCTCTTCTGAGCTCTCTGCAAGGCTTCACTAATGATGCTGATCTTT 600
 QY 602 ATTGTTGATGACCGTGGGATGAGGAGTCCATTTGTCGCTTTTATCTTATGCTTTT 661
 DB 601 ATTGTTGATGACCGTGGGATGAGGAGTCCATTTGTCGCTTTTATCTTATGCTTTT 660
 QY 662 ATTCTTTCAGATCTCGCGGTAGTCTGCTGAGGGAGGCTTAAGCTTCACTAGAC 721
 DB 661 ATTCTTTCAGATCTCGCGGTAGTCTGCTGAGGGAGGCTTAAGCTTCACTAGAC 720

DB 661 ATTCTTTCAGATCTCGCGGTAGTCTGCTGAGGGAGGCTTAAGCTTCACTAGAC 720
 QY 722 TGCACTCTCTACATTAATGAGATTTCTCTTTTCTTGGTCTGAGAGCTTTTACGACTC 781
 DB 721 TGCACTCTCTACATTAATGAGATTTCTCTTTTCTTGGTCTGAGAGCTTTTACGACTC 780
 QY 782 AAACCCCTTCCATTTTACCCCTGACACAGGGAAGTGTCTCTCTCTTCTATACCACT 841
 DB 781 AAACCCCTTCCATTTTACCCCTGACACAGGGAAGTGTCTCTCTCTTCTATACCACT 840
 QY 842 GTGTGCTCCATGTTTAACTTATCTACAGCTTGTAGAAATAGAGATGTCAAACTTGC 901
 DB 841 GTGTGCTCCATGTTTAACTTATCTACAGCTTGTAGAAATAGAGATGTCAAACTTGC 900
 QY 902 CTGAAGAGAACTTTTCCAGATTAAGCTTTCTTGAATAAATTTTACAAACAGAAAGA 961
 DB 901 CTGAAGAGAACTTTTCCAGATTAAGCTTTCTTGAATAAATTTTACAAACAGAAAGA 960
 QY 962 GA 963
 DB 961 GA 962

RESULT 3
 ADD12748
 ID ADD12748 standard; cDNA; 960 BP.

XX ADD12748;
 XX 01-JAN-2004 (first entry)
 XX
 DE cDNA encoding novel human olfactory receptor (OR) seq id 12.
 XX
 XX cardiant; antiarteriosclerotic; antidiabetic;
 KM G-protein Coupled Receptor modulator; gene therapy; olfactory receptor;
 KM G-protein Coupled Receptor X-associated disorder;
 KM GPCR associated disorder; cardiomyopathy; atherosclerosis;
 KM cell signal processing; metabolic pathway modulation; cancer; diabetes;
 KM human; G-protein coupled receptor; GPCR; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FN US2003109692-A1.
 XX
 PD 12-JUN-2003.
 XX
 PF 18-DEC-2001; 2001US-00023597.
 XX
 PR 18-DEC-2000; 2000US-0256635P.
 PR 21-DEC-2000; 2000US-0257876P.
 PR 04-JAN-2001; 2001US-0259743P.
 PR 10-JAN-2001; 2001US-0260718P.
 PR 12-JAN-2001; 2001US-0261498P.
 PR 24-JAN-2001; 2001US-0263469P.
 PR 08-FEB-2001; 2001US-0267464P.
 PR 22-FEB-2001; 2001US-0271021P.
 PR 14-MAR-2001; 2001US-0275946P.
 PR 23-MAR-2001; 2001US-0278150P.
 PR 18-APR-2001; 2001US-0284591P.
 PR 23-APR-2001; 2001US-0285718P.
 PR 19-JUN-2001; 2001US-0299327P.
 PR 16-AUG-2001; 2001US-0312902P.
 XX
 PA (PADI/) PADIGARU M.
 PA (KEKU/) KEKUDA R.
 PA (LIDL/) LI L.
 PA (BALD/) BALLINGER R A.
 PA (CASM/) CASMAN S J.
 PA (SPYT/) SPYTEK K A.
 PA (BAUM/) BAUMGARTNER J C.
 PA (BURG/) BURGESS C E.
 PI Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA,

PI Baumgartner JC, Burgess CE;
 XX WPI: 2003-801280/75.
 DR P-PSDB; ADD12749.
 XX
 PT New isolated olfactory receptor polypeptide for treating or preventing a
 PT G-Protein Coupled Receptor associated disorder e.g. cardiomyopathy or
 PT atherosclerosis.
 XX
 PS Claim 8; SEQ ID NO 23; 70bp; English.

CC The invention describes an isolated olfactory receptor polypeptide (I).
 CC (I) is used to identify an agent that binds to it by contacting (I) with
 CC the agent and determining binding. The agent is a cellular receptor or a
 CC downstream effector. (I) is also used to identify an agent that modulates
 CC the expression or activity of (I) by contacting a cell expressing (I)
 CC with the agent and determining whether the agent modulates expression or
 CC activity of (I). (I), or nucleic acid encoding (I), is used to treat or
 CC prevent a G-Protein Coupled Receptor (GPCR)-associated disorder in a
 CC subject, preferably a human, such as cardiomyopathy or atherosclerosis,
 CC or a disorder related to cell signal processing or metabolic pathway
 CC modulation. (I) is used to determine the presence or predisposition to a
 CC disease associated with altered levels of (I), preferably cancer, in a
 CC mammal. A nucleic acid encoding (I) is used to determine the presence or
 CC predisposition to a disease associated with altered levels of the nucleic
 CC acid, preferably cancer, in a mammalian subject. An antibody that binds
 CC to (I) is used to treat or prevent a GPCR-associated disorder, such as
 CC diabetes or a disorder related to cell signal processing and metabolic
 CC pathway modulation. An antibody that specifically binds (I) is used to
 CC determine the amount of (I) in a sample by contacting the sample with
 CC the antibody and determining the presence or amount of bound
 CC antibody. This sequence encodes a novel human olfactory receptor (OR), a
 CC G protein coupled receptor (GPCR).
 CC
 XX
 SQ Sequence 960 BP; 193 A; 247 C; 202 G; 318 T; 0 U; 0 Other;

Query Match 97.3%; Score 937; DB 9; Length 960;
 Best Local Similarity 99.7%; Pred. No. 3e-258;
 Matches 960; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 1 AATGGCTGCGGAGAACTCTCTCCGTCAGAGTTTATCCCGAGGCTTAATCCACA 60
 DB 1 AATGGCTGCGGAGAACTCTCTCCGTCAGAGTTTATCCCGAGGCTTAATCCACA 60
 QY 61 GCCGGGACTCCAGAGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 DB 61 GCCGGGACTCCAGAGTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
 QY 121 GGGGAACTGCGGCTTATATCTCTATAGGCTCAACTGCGCTGATATCCCAATGA 180
 DB 121 GGGGAACTGCGGCTTATATCTCTATAGGCTCAACTGCGCTGATATCCCAATGA 180
 QY 181 CTTTTCCTCCCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 DB 181 CTTTTCCTCCCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 QY 241 AATGCGATGAGTTTGTCTCAAGAGAACTTATCTCTCTCTCTCTCTCTCTCTCTCT 300
 DB 241 AATGCGATGAGTTTGTCTCAAGAGAACTTATCTCTCTCTCTCTCTCTCTCTCTCT 300
 QY 301 GTTCT 360
 DB 301 GTTCT 360
 QY 361 GACCGCTGAGGAGATCTTAAACCACTGTTGACAGATCAACCAATGTCCTCCAGGT 420
 DB 361 GACCGCTGAGGAGATCTTAAACCACTGTTGACAGATCAACCAATGTCCTCCAGGT 420
 QY 421 GTTCT 480
 DB 421 GTTCT 480
 QY 481 AGGAATATATGTTTCTCACTTTTGTGACAGACACTTGTCAATCACTATCATGTGGA 540

DB 480 AGGAATATATGTTTCTCACTTTTGTGACAGACACTTGTCAATCACTATCATGTGGA 537
 QY 541 CATCTCTCCCTCTCTGAGCTCTCTCTGACAGGCTCTTACATAAATGCTCTGATCTT 600
 DB 538 CATCTCTCCCTCTCTGAGCTCTCTCTGACAGGCTCTTACATAAATGCTCTGATCTT 597
 QY 601 TATGTTGACCGTTGAGCATTTGGGAGGCGCATTTGGCGCTTTTATCTTATGTTT 660
 DB 598 TATGTTGACCGTTGAGCATTTGGGAGGCGCATTTGGCGCTTTTATCTTATGTTT 657
 QY 661 TATCTCTGACCATTTCTCCGCTTATGTTCTGAGGAGGCTTAAAGCTTCACTAG 720
 DB 658 TATCTCTGACCATTTCTCCGCTTATGTTCTGAGGAGGCTTAAAGCTTCACTAG 717
 QY 721 CTGAGCTCTCAATAATGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 DB 718 CTGAGCTCTCAATAATGAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 777
 QY 781 CAAACCCCTCTCTCAATTTTACCCCTGACAGGAGAAAGTCTCTCTCTCTCTCTCT 840
 DB 778 CAAACCCCTCTCTCAATTTTACCCCTGACAGGAGAAAGTCTCTCTCTCTCTCTCT 837
 QY 841 TGTGTTGCGCATGTTTAAACCATTAATCTACAGCTGAGGAAATPAAGATGCAACTTGC 900
 DB 838 TGTGTTGCGCATGTTTAAACCATTAATCTACAGCTGAGGAAATPAAGATGCAACTTGC 897
 QY 901 CCTGAAGAGAACTTTTCCAGAAATAGCTTTCTTGAAAAAATTTTGAACAGAAAG 960
 DB 898 CCTGAAGAGAACTTTTCCAGAAATAGCTTTCTTGAAAAAATTTTGAACAGAAAG 957
 QY 961 AGA 963
 DB 958 AGA 960

RESULT 4
 AD86616
 ID AD86616 standard; DNA; 931 BP.
 XX
 AC AD86616;
 XX
 DT 01-JUN-2004 (first entry)
 XX
 DE Human GPCR gene SEQ ID NO:1069.
 XX
 DS ds: gene; human; GPCR;
 XX
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP1270724-A2.
 XX
 PD 02-JUN-2003.
 XX
 PF 18-JUN-2002; 2002EP-00013517.
 XX
 PR 18-JUN-2001; 2001JP-00246789.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 PI Suwa M, Aseai K, Akiyama Y, Aburatani H;
 XX
 DR WPI: 2003-315783/31.
 DR P-PSDB; AD86617.
 XX
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 PS Claim 1; SEQ ID NO 1069; 28bp; English.

CC The invention relates to a novel polynucleotide encoding a guanosine
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 CC the invention may have a use in gene therapy. The polynucleotide and
 CC polypeptide are useful for preparing a composition for treating a patient
 CC in need of increased or suppressed activity or expression of the
 CC guanosine triphosphate-binding protein coupled receptor. The
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
 CC invention.

XX
 SQ Sequence 931 BP; 202 A; 215 C; 180 G; 334 T; 0 U; 0 Other;

Query Match 78.4%; Score 755.4; DB 9; Length 931;
 Best Local Similarity 99.9%; Pred. No. 3.9e-206;
 Matches 756; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 207 TAGATTTAGTTCTACAGACATCATTCCTCCAAATAAGAGAGATTGTCAGAGA 266
 DB 1 TAGATTTAGTTCTCTACAGACATCATTCCTCCAAATAAGAGAGATTGTCAGAGA 60
 QY 267 AGAATATTATTTCTTACAGAGGATGATGATGATGATGATGATGATGATGATGAT 326
 DB 61 AGAATATTATTTCTTACAGAGGATGATGATGATGATGATGATGATGATGATGAT 120
 QY 327 TTTCGAGTCTTATCTGTCGAGGATGATGATGATGATGATGATGATGATGATGAT 366
 DB 121 TTTCGAGTCTTATCTGTCGAGGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 387 CACTGTGTACAGACATCATTCCTCCAAATAAGAGAGATTGTCAGAGA 446
 DB 181 CACTGTGTACAGACATCATTCCTCCAAATAAGAGAGATTGTCAGAGA 240
 QY 447 ACGGATGAGGATTTTGGGCTGATGATGATGATGATGATGATGATGATGATGAT 506
 DB 241 ACGGATGAGGATTTTGGGCTGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 507 GTGACAGACATTTCTTACAGAGGATGATGATGATGATGATGATGATGATGATGAT 566
 DB 301 GTGACAGACATTTCTTACAGAGGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 567 GCAAGGCTCTTACAGACATTCCTCCAAATAAGAGAGATTGTCAGAGA 626
 DB 361 GCAAGGCTCTTACAGACATTCCTCCAAATAAGAGAGATTGTCAGAGA 420
 QY 627 TGCCATTTGTCGAGGATGATGATGATGATGATGATGATGATGATGATGAT 686
 DB 421 TGCCATTTGTCGAGGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 687 GTTCGCTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 746
 DB 481 GTTCGCTGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 747 CTCTTTTCTTGGTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 806
 DB 541 CTCTTTTCTTGGTCTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 807 ACCAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866
 DB 601 ACCAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 867 TCTACAGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 926
 DB 661 TCTACAGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 927 GCTTTTCTTGAATAAATTTTGAATAAATTTTGAATAAATTTTGAATAA 963
 DB 721 GCTTTTCTTGAATAAATTTTGAATAAATTTTGAATAAATTTTGAATAA 757

RESULT 5
 AAH31668
 ID AAH31668 standard; DNA; 935 BP.
 XX
 AC AAH31668;

XX
 DT 30-JUL-2001 (first entry)
 XX
 DE Human olfactory receptor polynucleotide, SEQ ID NO: 241.
 XX
 XX Human olfactory receptor; OR; primary scent determination;
 KM secondary scent determination; polypeptide library; odour receptor;
 KM scent profile; scent fingerprint; scent representation; de.
 XX
 XX Homo sapiens.

PN WO200127158-A2.

PF 06-OCT-2000; 2000WO-US027582.

PR 08-OCT-1999; 99US-0158615P.

PR 24-FEB-2000; 2000US-0184809P.

PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.

PS Claim 8; Page 273; 1857bp; English.

CC The present sequence is one of a number of isolated polynucleotides which
 CC encode polypeptides involved in olfactory sensation. The polynucleotides
 CC can be used in screening for olfactory agonists and antagonists. The
 CC methods allow for the determination of primary scents and the
 CC identification of the odour receptors used to detect these primary
 CC scents. The methods also enable determination of secondary scents and the
 CC identification of combinations of odour receptors that are involved in
 CC detecting such secondary scents. This enables the construction of a scent
 CC representation (also called a scent fingerprint or scent profile), which
 CC may be used to re-create and edit scents. Libraries of olfactory
 CC receptors are useful for determining the interaction pattern of a
 CC composition with the receptors, and can be used for determining of a
 CC differences in the olfactory faculties of different individuals

SQ Sequence 935 BP; 189 A; 238 C; 190 G; 318 T; 0 U; 0 Other;

Query Match 78.0%; Score 751; DB 4; Length 935;
 Best Local Similarity 88.9%; Pred. No. 7.2e-205;
 Matches 835; Conservative 0; Mismatches 100; Indels 4; Gaps 2;

QY 2 ATGAGCTCCGAGAACTCTCTCTGAGAGAGATTATCTGCAAGGCTTAATCCACAG 61
 DB 1 ATGAGCTCCGAGAACTCTCTCTGAGAGAGATTATCTCTGCAAGGCTTAATCCACAG 60
 QY 62 CCGGAGATCCAGAGTCCCGCTTCTTCTGATGATGATGATGATGATGATGATGATGAT 121
 DB 61 CCGGAGATCCAGAGTCCCGCTTCTTCTGATGATGATGATGATGATGATGATGATGAT 120
 QY 122 GGAAGCTGGGCTTGAATATCTGATAGGCTCAATCTGCTGATATCCCAATGATC 181
 DB 121 GGAAGCTGGGCTTGAATATCTGATAGGCTCAATCTGCTGATATCCCAATGATC 180
 QY 182 TTTTCCCTTCAACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 241
 DB 181 TTTTCCCTTCAACTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 240
 QY 242 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 301
 DB 241 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 297
 QY 302 TTCTTTCTTCTGCTTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 361

PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.

XX
XX (CURAGEN CORP.)
PA
PI Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA,
PI Casan SL, Venne CM, Sheny SE, Gusev V, Malyskar UM, Edinger SJ,
PI Gerlach V, Smitson G, Stone DJ, Sciore P, MacDougall JR, Gunther E,
PI Peyman JA, Ellerman K, Gangoli EA, Millet I;
XX
XX WPI; 2002-59789/64.
DR P-SDB; ABG76802.

PT New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
in humans.

XX
XX Claim 1; Page 118; 685pp; English.

PS The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterine cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Alzheimers hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. AB558747-AB559231 represent human
CC GPCR coding sequences, primers and probes of the invention

XX
XX Sequence 991 BP; 205 A; 270 C; 198 G; 318 T; 0 U; 0 Other;

SQ Query Match 72.1%; Score 694.2; DB 6; Length 991;
Best Local Similarity 83.7%; Pred. No. 1.5e-188;
Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 8 GCCGAGAACCTCCTCCCGTGAAGAAGTTATTCCTGCACGGCTTATATCACCAAGCCGGGA 67
Db GCACCACAAAACCTCTGTGAAGAAGTTATTCCTGGAAGGCTTAAACCAACAGCCGGGA 111

QY 68 CTCAGGCTCCCCT 127
Db CTGCGGATCCCCCT 171

QY 128 CTGGGCTTAATACTCTGATAGGCTCAACTCTGCCCTGCATATCCCATCTACTTTTTC 187
Db CTGGGCTTAATACTCTGATAGGCTCAACTCTGCCCTGCATATCCCATCTACTTTTTC 231

QY 188 CCCTTGAACTGACCTCGTAGATTGTTAGTTTCTCTAGACATCATCCCAAATGCTG 247
Db CTTTTTAACCTCTTTAATATTTCTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 291

QY 248 ATAGATTGTTCTGAAGAAGAACTTATTTCTTACAAGGCTGTATAGTCACTTCTTC 307

Db 292 ATGAGTTTGTCTCAGAGAGAAACATCATTTCTTTCACAGGGGTGTATGACTCAGCTCTTC 351
QY 308 TTCTCTGTGTTCTGTTCTTTCTGATGCTTCATCCGTGTGGGAGATGTGAGAGACCGC 367
Db 352 TTCTCTGTGTTCTGTTCTGTCTGTGATGCTTCATCCGTGTGAGGATGTGAGAGACCGC 411
QY 368 TACGTGGGATGTGATGACCACTGTTGTACAGATGATGATGATGATGATGATGATGATG 427
Db 412 TACGTGGGATGTGATGACCACTGTTGTACAGATGATGATGATGATGATGATGATGATG 471
QY 428 CTCTCTTTTACGTTGTTCTGATGAGGATGTTGGGGGTTTGGGGGTTTGGGGGTTTGGGG 487
Db 472 CTCTCTTTTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 531
QY 488 ATAGTGTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547
Db 532 ATAGTGTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591
QY 548 CCCCTCTTGTGATGCTCTCTGCAACGGCTTTTCAATATGCTGATGATGATGATGATGATG 607
Db 592 CCTCTCTTGTGATGCTCTCTGCAACGGCTTTTCAATATGCTGATGATGATGATGATGATG 651
QY 608 GTGACCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
Db 652 GTGACCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
QY 668 TCCAGCATTTCCCGGTTAGTTCTGCTGATGAGGAGATGATGATGATGATGATGATGATG 727
Db 712 TCCAGCATTTCCCGGTTAGTTCTGCTGATGAGGAGATGATGATGATGATGATGATGATG 771
QY 728 TCCAGCATTTCCCGGTTAGTTCTGCTGATGAGGAGATGATGATGATGATGATGATGATG 787
Db 772 TCCAGCATTTCCCGGTTAGTTCTGCTGATGAGGAGATGATGATGATGATGATGATGATG 831
QY 788 CCTCTCTTGTGATGCTCTCTGCAACGGCTTTTCAATATGCTGATGATGATGATGATGATG 847
Db 832 CCTCTCTTGTGATGCTCTCTGCAACGGCTTTTCAATATGCTGATGATGATGATGATGATG 891
QY 848 CCCATGTTTAAACCATTAATCTACAGCTGAGGATGATGATGATGATGATGATGATGATG 907
Db 892 CCCATGTTTAAACCATTAATCTACAGCTGAGGATGATGATGATGATGATGATGATGATG 951
QY 908 AGAAGCTTTTCCAGATTAAGCTTTCTGATGATGATGATGATGATGATGATGATGATG 946
Db 952 AGAAGCTTTTCCAGATTAAGCTTTCTGATGATGATGATGATGATGATGATGATGATG 990

RESULT 7
ID ADC85838 standard; DNA; 1333 BP.
XX
AC ADC85838;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human GPCR gene SEQ ID NO:291.
XX
KM de; gene; human; GPCR;
XX
XX guanine triphosphate-binding protein coupled receptor; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1270724-A2.
XX
PD 02-JAN-2003.
XX
PF 18-JUN-2002; 2002EP-00013517.
XX
PR 18-JUN-2001; 2001JP-00246789.
XX
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

PI Suwa M, Arai K, Akiyama Y, Aburatani H;
XX
XX WPI; 2003-315783/31.
DR P-PSDB; ADC85839.
XX
XX
PT New polynucleotide, useful for preparing a composition for treating a
PT patient in need of increased or suppressed activity or expression of the
PT guanine triphosphate-binding protein coupled receptor.
XX
XX
PS Claim 1, SEQ ID NO 291; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
CC the invention may have a use in gene therapy. The polynucleotide and
CC polypeptide are useful for preparing a composition for treating a patient
CC in need of increased or suppressed activity or expression of the
CC guanine triphosphate-binding protein coupled receptor. The
CC polynucleotide sequences shown in ADC8548-ADC87616 encode GPCR's of the
CC invention.
SQ Sequence 1333 BP; 296 A; 327 C; 268 G; 442 T; 0 U; 0 Other;
Query Match 72.1%; Score 694.2; DB 9; Length 1333;
Best Local Similarity 83.7%; Pred. No. 1,7e-188;
Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;
QY 8 GCCGAGAACCTCCCTCCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 67
Db 204 GCAGCCAAAACCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 263
QY 68 CTCAGGATCCCGCTCTTCT 127
Db 264 CTCAGGATCCCGCTCTTCT 323
QY 128 CTGGGCTGTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187
Db 324 CTGGGCTGTTAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 383
QY 384 CTCTTAAACCTCTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 443
Db 444 ATGAGTTTGTCTCAGAGAGAAACATCATTTCTTTCACAGGGGTGTATGACTCAGCTCTTC 503
QY 248 ATGAGTTTGTCTCAGAGAGAAACATCATTTCTTTCACAGGGGTGTATGACTCAGCTCTTC 307
Db 444 ATGAGTTTGTCTCAGAGAGAAACATCATTTCTTTCACAGGGGTGTATGACTCAGCTCTTC 503
QY 308 TTCTCTGTGTTCTGTTCTTTCTGATGCTTCATCCGTGTGAGGATGTGAGAGACCGC 367
Db 504 TTCTCTGTGTTCTGTTCTTTCTGATGCTTCATCCGTGTGAGGATGTGAGAGACCGC 563
QY 368 TACGTGGGATGTGATGACCACTGTTGTACAGATGATGATGATGATGATGATGATGATGATG 427
Db 564 TACGTGGGATGTGATGACCACTGTTGTACAGATGATGATGATGATGATGATGATGATGATG 623
QY 428 CTCTCTTTTACGTTGTTCTGATGAGGATGTTGGGGGTTTGGGGGTTTGGGGGTTTGGGG 487
Db 624 CTCTCTTTTGTGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 683
QY 488 ATAGTGTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547
Db 684 ATAGTGTGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 743
QY 548 CCCCTCTTGTGATGCTCTCTGCAACGGCTTTTCAATATGCTGATGATGATGATGATGATG 607
Db 744 CCTCTCTTGTGATGCTCTCTGCAACGGCTTTTCAATATGCTGATGATGATGATGATGATG 803
QY 608 GTGACCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 667
Db 804 GTGACCGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 863
QY 668 TCCAGCATTTCCCGGTTAGTTCTGCTGATGAGGAGATGATGATGATGATGATGATGATGATG 727
Db 864 TCCAGCATTTCCCGGTTAGTTCTGCTGATGAGGAGATGATGATGATGATGATGATGATGATG 923

QY 728 TCCTACATTAATGCAATTTCTCTTTCTTTGGGTCAGAGCTTTTACGACTCAAAACC 787
Db 924 TCCACATATATATGATTTCTTTCTTTGGTTCGGTTCATTATGATCAATCAACC 983
QY 788 CCTTCATTTTACCCTGGACAGGGGAAAGTCTCTCTCTTTCTATCCACTGTGTG 847
Db 984 CTTTCATCTCTGCTCCCTCAGCAAGGAAAGTCTCTCTCTTTCTATACATTAATGATC 1043
QY 848 CCCATGTTTAAACCATTAATCTACAGCTGAGAAATTAAGATGTCAAACTTCCCTGAAG 907
Db 1044 CCGGTGTTAAACCATTAATCTATAGCTTGAGAACCAAGATGTCAAACTTCCCTGAAG 1103
QY 908 AGAACCTTTTCCAGATTAAGCTTTTCTTGAATAAAATTT 946
Db 1104 AGAACCTTTGAGCAAGAAATCTTTTCTTAAGAAAGATT 1142

RESULT 8
ABK97207
ID ABK97207 standard, cDNA; 976 BP.
AC ABK97207;
XX
XX 07-OCT-2002 (first entry)
DE Human G-protein coupled receptor (GPCR) GPCR gene #1.
XX
XX G-protein coupled receptor; receptor; GPCR; GPCR; cardiomyopathy;
KW atherosclerosis; diabetes; cell signal processing; cancer; trauma;
KW metabolic pathway; modulation; neuro-olfactory system; surgery;
KW neoplastic disorder; adenocarcinoma; lymphoma; prostate cancer;
KW uterine cancer; immune response; acquired immunodeficiency syndrome; AIDS;
KW asthma; Crohn's disease; multiple sclerosis;
XX Albright hereditary osteodystrophy; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX WO200250117-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US049077.
XX
XX 18-DEC-2000; 2000US-0256635P.
XX 21-DEC-2000; 2000US-0257876P.
XX 04-JAN-2001; 2001US-0259743P.
XX 10-JAN-2001; 2001US-0260718P.
XX 12-JAN-2001; 2001US-0261498P.
XX 24-JAN-2001; 2001US-0263689P.
XX 08-FEB-2001; 2001US-0267464P.
XX 22-FEB-2001; 2001US-0271021P.
XX 14-MAR-2001; 2001US-0275946P.
XX 23-MAR-2001; 2001US-0278150P.
XX 18-APR-2001; 2001US-0284591P.
XX 23-APR-2001; 2001US-0285718P.
XX 19-JUN-2001; 2001US-0293327P.
XX 16-AUG-2001; 2001US-0312902P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Padigam M, Kehuda R, Colman SD, Splytek KA, Ballinger RA,
PI Vermet CAM, Li L, Shenoy S, Casman SJ,
XX WPI; 2002-528447/56.
XX P-PSDB; ABG68134.
XX
XX New G-protein coupled receptor polypeptides for treating or preventing
PT cardiomyopathy, atherosclerosis, diabetes, multiple sclerosis, acquired
XX immunodeficiency syndrome or cancer in humans.
XX
XX Claim 5; Page 79; 110pp; English.

CC The present invention relates to a new G-protein coupled receptor (GPCR) CC
CC polypeptide. The GPCR polypeptide, GPCR nucleic acid and antibody are CC
CC useful for treating, preventing or alleviating a GPCR-associated CC
CC disorder or a pathological state in a subject, particularly a human. In CC
CC particular, the disorder is cardiomyopathy, atherosclerosis, diabetes, or CC
CC a disorder related to cell signal processing and metabolic pathway CC
CC modulation. The GPCR polypeptide and nucleic acid are also useful for CC
CC diagnosing the presence of or predisposition to a disease associated with CC
CC altered levels of GPCR, particularly cancer. The GPCR nucleic acid and CC
CC polypeptide are especially useful in therapeutic or prophylactic CC
CC applications for disorders of the neuro-olfactory system, e.g. those CC
CC induced by trauma, surgery and/or neoplastic disorders. The DNA encoding CC
CC the protein is useful in gene therapy for treating the above conditions. CC
CC Furthermore, the nucleic acids and polypeptides are useful in treating CC
CC adenocarcinoma, lymphoma, prostate cancer, uterine cancer, immune CC
CC response, acquired immunodeficiency syndrome (AIDS), asthma, Crohn's CC
CC disease, multiple sclerosis or Albright hereditary osteodystrophy. These CC
CC are also useful in developing powerful assay system for functional CC
CC analysis of various human disorders, as well as in diagnostic CC
CC applications. The present nucleic acid sequence represents one of a CC
CC collection (ABK97207-ABK97226) of human GPCR genes that encode the human CC
CC GPCR proteins (AAV68134-AAV68153) of the invention CC
XX

SO Sequence 976 BP; 204 A; 259 C; 204 G; 309 T; 0 U; 0 Other;
Query Match 72.0%; Score 693; DB 6; Length 976;
Best Local Similarity 83.5%; Pred. No. 3.3e-188;
Matches 786; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 1 AATGCTGCGGAGAACTCCTCTCCGTACAGATTTATCCCGAGCTTATCCACCA 60
Db 7 AATGCGCCAGCCCAAAATCTCTGTGACAGATTTATCCCGAGCTTATCCACCA 66
QY 61 GCGGAGCTCAGATCCCGCTCTCTCTCTTTTGAAGTTCTACGGGCTACGGTGT 120
Db 67 GCGGAGCTCAGATCCCGCTCTCTCTCTCTTTTGAAGTTCTACGGGCTACGGTGT 126
QY 121 GGGGAACCTGGGCTTGAATATCTGATAGGCTCACTGTGCTGATATCCCATGTA 180
Db 127 GGGGAACCTGGGCTTGAATATCTGATAGGCTCACTGTGCTGATATCCCATGTA 186
QY 181 CTTTTCCTCCCACTGCTCCCTGATATTTAGTTTCTCTAGACCATCATTTCCCA 240
Db 187 CTTTTCCTCCCACTGCTCCCTGATATTTAGTTTCTCTAGACCATCATTTCCCA 246
QY 241 AATGCTGATGATTTGTCTCAAGAGAACATTAATCTCTCAAGGCTGATGATCA 300
Db 247 AATGCTGATGATTTGTCTCAAGAGAACATTAATCTCTCAAGGCTGATGATCA 306
QY 301 GTTCTTCT 360
Db 307 GTTCTTCT 366
QY 361 GACCGCTAGTGGGCTATGTAAACCACTGTTGACAGATCAATGTCCTCCAGGT 420
Db 367 TGACCGCTAGTGGGCTATGTAAACCACTGTTGACAGATCAATGTCCTCCAGGT 426
QY 421 GTGTTGCT 480
Db 427 GTGTTGCT 486
QY 481 AGAAATATAGTGTCTCACTTTGTGACAGACCACTTGTCACTACATAGTGTGA 540
Db 487 AGAAATATATGAACCGATCTCTGTGCTGAGAACCTTGTCACTATTTCAATGTGA 546
QY 541 CATCTTCCCTTTTGTAGCTCTCTGCAACGGCTCTTAATAAATGCTGTGATCTT 600
Db 547 CATCTTCCCTTTTGTAGCTCTCTGCAACGGCTCTTAATAAATGCTGTGATCTT 606
QY 601 TATGTTGTGACCTTGGCATTTGGGGTGGCCATTTGTCGCTTTTATCTTATGTTT 660
Db 607 TATGTTGTGCTTTGACCTTGGCATTTGGGGTGGCCATTTGTCGCTTTTATGTTT 666

Qy	66	TATCTCTTCAGCAATTCCTCGGATGTCTGCTGAGGCAAGTCTTAAGCTTCAGTAG	720
Db	667	CATCTCTCCAGCATTCCTACACAAAGTCTACAAAGGCAAGTCCAAAGCTTTAGTAC	720
Qy	721	CTGCACTCTCTACATAATATGCACTTCTCTTTCTTTGGGTGACAGCTTTTACGTACT	780
Db	727	TTGCAAGTTCCACATAATATGATTTCTCTTTCTTTGGTCTGTGCTTTCACGTATCT	780
Qy	781	CAAAACCCCTTCATTTTACCCCTGAGCAGGGAAGATGTCCTCCTGTTCTATACAC	840
Db	787	CAAAACCCCTTTCATCTCTGCGCCCTGAGCAAGGAAGATGTCCTCCTGTTCTATACAT	840
Qy	841	TGTGATGCCATGTGTTTACCCATTATCTACAGCTGAGGAATATGATGTCAACTTGC	900
Db	847	AATAGTCCCGGTGTAAACCATATATCTATGCTTGAGGAACAAGGATGTCAAGTTGC	900
Qy	901	CTGGAAGAACCTTTTCCGAAATAGTCTTTCTTGAAAA 941	
Db	907	CTGAGAGAACCTTTGGGCGCAAAAAATCTTTCTTAAAGAA 947	
RESULT 9			
AD60328			
ID	AD60328	standard; DNA; 976 BP.	
AC	AD60328;		
XX			
DT	18-DEC-2003	(first entry)	
DE			
XX			
XX		Human G-Protein coupled receptor (GPCR) GPCRX DNA #1.	
KM		Human; G-protein coupled receptor; GPCRX; stroke; obesity; virulence;	
KW		multiple sclerosis; Alzheimer's disease; graft-versus-host disease;	
KM		endometriosis; tissue typing; gene therapy; vaccine; antibacterial;	
KW		retinal disease; infectious disease; bulimia; receptor; fungicide;	
KM		Parkinson's disease; hypertension; acute heart failure; infection;	
KW		cardiomyopathy; atherosclerosis; diabetes; detectability disorder;	
KM		cancer; signal transduction pathway disorder; metabolic disorder;	
KW		developmental disorder; osteoporosis; protozoacide; asthma; gene; ds.	
XX			
OS		Homo sapiens.	
XX			
FT	Key	Location/Qualifiers	
FT	CDS	8..943	
FT		/*tag= a	
FT		/product= "Human GPCRX protein"	
XX			
XX		US2003100491-A1.	
XX			
PD	29-MAY-2003.		
XX			
PF	18-DEC-2001; 2001US-00024399.		
XX			
PR	18-DEC-2000; 2000US-0256635P.		
PR	21-DEC-2000; 2000US-0257876P.		
PR	04-JAN-2001; 2001US-0259743P.		
PR	10-JAN-2001; 2001US-0260718P.		
PR	12-JAN-2001; 2001US-0261498P.		
PR	24-JAN-2001; 2001US-0263689P.		
PR	08-FEB-2001; 2001US-027464P.		
PR	22-FEB-2001; 2001US-0271021P.		
PR	14-MAR-2001; 2001US-027596P.		
PR	23-MAR-2001; 2001US-0278150P.		
PR	18-APR-2001; 2001US-0284591P.		
PR	23-APR-2001; 2001US-0285718P.		
PR	19-JUN-2001; 2001US-029337P.		
PR	16-AUG-2001; 2001US-0312902P.		
XX			
PA	(PADI/)	PADIGARU M.	
PA	(KERU/)	KERUDA R.	
PA	(COLM/)	COLMAN S. D.	
PA	(SPYT/)	SPYTER K. A.	
PA	(BALL/)	BALLINGER R. A.	

PA	(VERN/) VERNET C A M.
PA	(LIIL/) LI L.
PA	(SHEN/) SHENOY S G.
PA	(CASMAN/) CASMAN S J.
P1	Padigaru M., Rekuda R., Colman SD, Spytek KA, Ballinger RA,
P1	Vernet CM, Li Lu, Shenoy SG, Casman SJ;
XX	WPI; 2003-755210/71.
DR	P-PsDB; AAA39659.
XX	
PT	New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,
PT	useful for diagnosis, preventing or treating GPCR-associated disorders,
PT	e.g. cardiomyopathy, atherosclerosis, cancer or diabetes, and in
PT	pharmacogenomics.
XX	
PS	Claim 8; Page 32; 46pp; English.
XX	
CC	The invention relates to G-protein coupled receptor (GPCR) polypeptides
CC	(designated as GPCR) and nucleic acid sequences. GPCR polypeptides,
CC	nucleic acids and antibodies are useful in diagnosing, preventing or
CC	treating GPCR-associated disorders, such as cardiomyopathy, diabetes,
CC	atherosclerosis and cancer. These may also be used for treating or
CC	preventing other diseases like developmental disorders, taste and scent
CC	detectability disorders, signal transduction pathway disorders, retinal
CC	diseases, metabolic disorders (e.g. obesity), infectious diseases (e.g.
CC	bacterial, fungal, protozoal or viral infections), bulimia, asthma,
CC	Parkinson's disease, hypertension, acute heart failure, osteoporosis,
CC	multiple sclerosis, Alzheimer's disease, stroke, graft-versus-host
CC	disease or endometriosis. GPCR nucleic acid is used as hybridisation
CC	probes, in chromosome mapping, tissue typing, preventive medicine and
CC	pharmacogenomics. It is also useful in gene therapy. GPCR is useful as
CC	vaccines. The present sequence is human GPCR DNA
XX	
SQ	Sequence 976 BP; 204 A; 259 C; 204 G; 309 T; 0 U; 0 Other;
	Query Match 72.0%; Score 693; DB 9; Length 976;
	Best Local Similarity 83.5%; Pred. No.3,36-188;
	Matches 786; Conservative 0; Mismatches 155; Indels 0; Gaps 0
QY	1 AATGGTGCAGCAAACTCCTCTCCGACAGAGTTAATCCTCGACGGATTATCCACCA 60
DB	7 AATGGGCCAGCCCAAACCTCTTCGTACAGAGTTATCTCGAAGGCTTAACCCACA 66
QY	61 GCCGGACTCCAGAGTCCCCGCTTCTCCGCTTCTCTAGCTTTTACGGCGTACCGTGCT 120
DB	67 GCGGGAGCTCGGAGATCCCCTCTTCTCTCTCTCTCTGAGTTTACACGGTACCCTGAT 126
QY	121 GGGAACCTGGGCTTGATATCTCGATAGGGCTCACTCTCGGCTCATATCCCATATGA 180
DB	127 GGGAACCTGGGCTTGATATCCGTAGTGGGCTGAATCTCACCTGCACCTCCCATGTA 186
QY	181 CTTTTTCCCCTTCACCTGTCCCTCGTAGATTATAGTTTCTTCAGACATCATTTCCCA 240
DB	187 CTCTCTCTTTTAACTCTCTCTTAAATGATTTCTGTTTCCACATCACTATCTCCCA 246
QY	241 AATGCTGATGAGTTTGTCTCAAGGAAGAATATTTCTTCACAGGGTATGATGATA 300
DB	247 AATGCTGATGAGTTTGTCTCAAGGAAGAATATTTCTTCACAGGGGTATGACTCA 306
QY	301 GTCT 360
DB	307 GCT 366
QY	361 GAGCGGCTACGATGGGCAATCTGTAAACCACTGTGTACAGATCAACCAATCTTCCAGGT 420
DB	367 TGACCCGCTACGATGGGCAATCTGTAAACCACTGTGTACAGATCAACCAATCTTCCAGGT 426
QY	421 GTGTTTGACCTTTTACTAGGGGTATACGGGATGGGGGTTTGGGGCTGTGGCTCATAC 480
DB	427 GTGTTTGACCTTTTGTGTGGGTCTATAGGATGGGGTGTGTGTGGGGCATGGCCACAC 486
QY	481 AGGAATATATAGTTTCTACCTTTGTGCAGACACCTTGTCATATCTACATGTGTGA 540

Db 487 AGGAGCATATGACCTGACCTTCTGTCTGACGACCTTTCATCATTTTCATCTGGA 546
 Qy 541 CATCTTCCCTCTTGTAGCTCTCTGCAACGCTTTTCAATATGTCCTGATCTT 600
 Db 547 CATCTTCCCTCTTGTAGCTCTCTGCAACGCTTTTCAATATGTCCTGATCTT 606
 Qy 601 TATGTTGATGACCTGATGAGCTGGGCTGACATGTCCTTTTATCTTATGAGTT 660
 Db 607 TATGTTGATGAGCTGATGAGCTGGGCTGACATGTCCTTTTATCTTATGAGTT 666
 Qy 661 TATCTTTCAGCATCTCTGCGCTTATGTCCTGAGGAGGCTTAAAGCTTCACTG 720
 Db 667 CATCTTCCCTCTTGTAGCTCTCTGCAACGCTTTTCAATATGTCCTGATCTT 726
 Qy 721 CTGAGCTCTTACATATGACCTTTCTTCTTCTTGTGAGGAGCTTATGATCTT 780
 Db 727 TTGAGTTCCCATATATGATGATTTCTTTCTTTGTTGTTGCTTTCATGATCTT 786
 Qy 781 CAATCCCTCTTCAATTTTACCTCTGACGAGGAGAAAGTCTCTCTCTTCTATACAC 840
 Db 787 CAATCCCTCTTCAATCTCTGCGCTTCTGAGGAGGAGAAAGTCTCTCTCTATACAT 846
 Qy 841 TGTGTCCTCATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 900
 Db 847 AATAGTCCCTGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 906
 Qy 901 CCTGAGAGACCTTTTCCAGAAATTAAGCTTTTCTTGAATA 941
 Db 907 CCTGAGAGAGACCTTTTCCAGAAATTAAGCTTTTCTTGAATA 947

RESULT 10
 ABT05655
 ID ABT05655 standard; DNA: 953 BP.
 AC ABT05655;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE GPCR 4 protein encoding DNA SEQ ID NO 13.

XX
 KM Anti-diabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCRX;
 KM antiparkinsonian; cardiast; antiarteriosclerotic; immunosuppressive;
 KM hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;
 KM anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;
 KM diabetes; metabolic disorder; diabetes; obesity; infectious disease;
 KM anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidemia;
 KM Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;
 KM metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasm;
 KM congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
 KM transplantation; adenoleukodystrophy; congenital adrenal hyperplasia;
 KM prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
 KM hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
 KM graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
 KM multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;
 KM gene therapy; transgenic animal; gene; de.

XX
 OS Unidentified.
 XX
 PN WO200246229-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US046530.
 XX
 PR 05-DEC-2000; 2000US-0251459P.
 PR 29-DEC-2000; 2000US-0259007P.
 PR 04-DEC-2001; 2001US-00005041.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Casmen SJ, Padigaru M, Burgess CE, Shimkets RA, Spyrek KA;

PI Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CM;
 PI Dickinson KS, Ballinger RA, Wolenc AR;
 XX
 DR MPI; 2002-537559/57.
 XX
 PT P-FSDB; AB004724.
 PT Novel isolated G-protein coupled receptor polypeptide, designated NOVX,
 PT useful for treating or preventing in human receptor-associated disorders
 PT e.g. cardiomyopathy, atherosclerosis or diabetes.
 XX
 PS Claim 9; Page 33; 264pp; English.

XX
 CC The invention relates to a novel isolated G-protein coupled receptor X
 CC (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide
 CC and the antibody of the isolated protein, its encoding polynucleotide
 CC preventing a GPCR-associated disorder in a subject, preferably human,
 CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The
 CC isolated protein, its encoding polynucleotide and the antibody of the
 CC isolated protein is useful for treating or preventing metabolic
 CC disorders, diabetes, obesity, infectious disease, anorexia,
 CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
 CC immune disorders, haematopoietic disorders, and various dyslipidaemias,
 CC metabolic disturbances associated with obesity, the metabolic syndrome X,
 CC wasting disorders associated with chronic diseases, and cancer. The
 CC disorders also include cardiomyopathy, atherosclerosis, hypertension,
 CC congenital heart defects, aortic stenosis, subaortic stenosis,
 CC transplantation, adenoleukodystrophy, congenital adrenal hyperplasia,
 CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
 CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
 CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial
 CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein,
 CC its encoding polynucleotide and the antibody of the isolated protein is
 CC useful in screening assays, detection assays (e.g., chromosomal mapping,
 CC tissue typing, forensic biology). The isolated polynucleotide is useful
 CC in gene therapy, to express the isolated protein, to detect GPCR mRNA or
 CC a genetic lesion in a GPCR gene, and to modulate GPCR activity. The
 CC cell of the invention is useful for producing non-human transgenic
 CC animals. This polynucleotide sequence represents DNA encoding a GPCR
 CC protein of the invention
 XX

XX
 SQ Sequence 953 BP; 202 A; 256 C; 193 G; 302 T; 0 U; 0 Other;

XX
 Query Match 71.9%; Score 692.4; DB 6; Length 953;
 Best Local Similarity 83.8%; Pred. No. 4.8e-188;
 Matches 783; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

Qy 8 GCCGGAACCTCCTCCGTCAGACAGTTATCTCGACAGCTTAATCCACAGCGGGA 67
 Db 19 GCAGCAAAACCTCTCTGTACAGATTTATCTCGAAGCTTAACCCACAGCGGGA 78
 Qy 68 CTCAGGTCCT 127
 Db 79 CTGCGGATCCCT 138
 Qy 128 CTGGGCTGATATGCTGATGAGGCTCACTCTGCTGATATGCCATGATCTTTT 187
 Db 139 CTGGGCTGATATGCTGATGAGGCTCACTCTGCTGATATGCCATGATCTTTT 196
 Qy 188 CCTTCAACTGTCCTGATGATTTAGTTTCTTACAGACCATTCATCCAAATGCTG 247
 Db 199 CTTTAACTCTCTTATATGATTTGTTTCTTCACTACATCACTCCCAAAATGCTG 258
 Qy 248 ATGAGTTTGTCTGAGGAACATATTTCTTCAAGAGGATGATGATGATGATGATG 307
 Db 259 ATGAGTTTGTCTGAGGAACATATTTCTTCAAGAGGATGATGATGATGATGATG 318
 Qy 308 TTTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 367
 Db 319 TTTCTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 378
 Qy 368 TACGAGGATCTGATACCACTGTTGATACAGTACATGTCCTCCAGAGGATGTTG 427
 Db 379 TACGAGGATCTGATACCACTGTTGATACAGTACATGTCCTCCAGAGGATGTTG 438

QY 428 CTCCTTTACTGAGTGTCTACCGGATGGGGGTTTGGGGGCTGTGCTCATACAGAAAT 487
 DB 439 CTCCTTTTGGGGGCTATGGGATGGGTTTGTGGGGCCATGGCCACAGAGAGC 498
 QY 488 ATAGTGTCTACCTTTTGGGACAGAACCTTGGCATCTCATAGTGTGACATCCTT 547
 DB 499 ATAAAGAACCTTACCTTGTGGTGAACAACCTTGTCAATCATTTATGTGACATCCTT 558
 QY 548 CCCCTTCTGAGCTCTCCCTGCAACGAGCTTTACATAAATGCTGGTCACTTTATGTT 607
 DB 559 CTTCTCTTGGAGCTCTCCGCAACAGCTTTACATGAATGAGCCGGTGTCTTTATGTG 618
 QY 608 GTGACCGTTGGCATTGGGGTGCCTCATTTGCTCCGCTTTTATCTCTTATGTTATTTCT 667
 DB 619 GTGGCTGTGAGCTTGAATGGCAATGGCAATGCTGCTGCTTTATTTCTTAAGCCCTCATCTC 678
 QY 668 TCCAGATCTCCGGGTTAGTCTGTGAGGAGGAGCTTAAGCCCTGAGTGTGAGC 727
 DB 679 TCCAGATCTTAACAACAGCTTCTACAGAGGAGGAGCTTAAGCCCTTATGTTGAGT 738
 QY 728 TCCATCATATGACAGTCTTCTTTTCTTTGGGTGAGAGCTTTTACCTCAACCC 787
 DB 739 TCCCATATATGATGTTCTCTTTTCTTTGGTGTGCTTGTGCTTATGATGATCAAAACC 798
 QY 788 CTTTCATTTTACCCCTGAGAGGAGGAGTCTCTCCCTGTTATACCACTGTGGTG 847
 DB 799 CTTTCATCTGCTCTGAGAGGAGGAGTCTCTCTCTTTCTATACATATAGTC 858
 QY 848 CCCATGTTTAAACCATTAATCTACAGCTGAGAGATGAGATGCAACTGCTGAAG 907
 DB 859 CCCGTTTAAACCATTAATCTATAGCTTGAAGAAACAGAGATGCAAGTCCCTGAGG 918
 QY 908 AGAACCTTTTCCAGATTAAGCTTTCTTGAATA 941
 DB 919 AGAACCTTTGGGAGAAATCTTTCTTGAATA 952
 RESULT 11
 AAS15910
 ID AAS15910 standard; cDNA; 933 BP.
 AC AAS15910;
 XX
 DT 25-JUN-2002 (first entry)
 XX
 DE DNA encoding G-protein coupled receptor (GPRC) #14.
 XX
 KW G-protein coupled receptor; GPRC; vaccine; gene therapy;
 KW cell proliferation disorder; cancer; arteriosclerosis;
 KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
 KW hypertension; ischemic heart disease; gastrointestinal disorder;
 KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
 KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
 KW schizophrenic disorder; neuroskeletal disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..933
 FT /*tag= a
 FT /product= "GPRC 14"
 FT /note= "G-protein coupled receptor 14"
 XX
 PN MO20016742-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 01-MAR-2001; 2001WO-US006814.
 XX
 PR 03-MAR-2000; 2000US-0186854P.
 PR 10-MAR-2000; 2000US-0188384P.
 PR 17-MAR-2000; 2000US-0190453P.

PR 20-MAR-2000; 2000US-0190730P.
 XX
 FA (INCYTE) INCYTE GENOMICS INC.
 XX
 PI Lal P, Tang YT, Paterson C, Yao MG, Shin LL, Tribouley CM;
 PI Lu DM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Hatland L;
 PI Walsh RT, Lo TP, Borowsky ML;
 XX
 DR WPI: 2001-656776/75.
 DR P-PSDE; AAU010313.
 XX
 PT Novel G-protein coupled receptor polypeptides, for treating and
 PT preventing autoimmune/inflammatory disorders, neurological disorders,
 PT cell proliferative disorders, cardiovascular disorders and viral
 PT infections.
 XX
 PS Claim 5, Page 138; 141pp; English.
 XX
 CC The invention describes a novel isolated polypeptide, selected from a
 CC group of 21 G-protein coupled receptor polypeptides (GPRC) and useful in
 CC vaccines and gene therapy. The polypeptide (I) is useful for screening
 CC for agonist or antagonist of (I), compounds specifically binding to (I),
 CC or compounds that modulate the activity of (I). The polynucleotide
 CC encoding (I) is useful for screening a compound for effectiveness in
 CC altering expression of a target polynucleotide comprising (II), by
 CC exposing a sample comprising the target polynucleotide to a compound,
 CC detecting altered expression of the target polynucleotide, and comparing
 CC the expression of the target polynucleotide in the presence of varying
 CC amounts of compound and in the absence of the compound. (I) and (II) are
 CC useful for diagnosis, treatment and prevention of cell proliferative
 CC disorders (e.g. cancer, arteriosclerosis, atherosclerosis), neurological
 CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
 CC neuroskeletal disorders), gastrointestinal disorders (e.g. anorexia,
 CC ischaemic heart disease), inflammatory disorders (e.g. diabetes mellitus,
 CC peptic ulcer), autoimmune/inflammatory disorders such as obesity,
 CC osteoporosis, psoriasis, and metabolic disorders such as detecting
 CC Furthermore, the polynucleotide is useful; as primers for detecting
 CC single nucleotide polymorphisms; as elements in microarray, to monitor or
 CC measure protein-protein interactions, drug-target interactions, and gene
 CC expression profiles; to generate a transcript image of a tissue or cell
 CC type, and to generate hybridisation probes useful in mapping the
 CC naturally occurring genomic sequence. This sequence encodes G-protein
 CC coupled receptor 14, one of 21 GPRC proteins described in the method of
 CC the invention
 XX
 SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
 XX
 Query Match 71.8%; Score 691.6; DB 5; Length 933;
 Best Local Similarity 84.0%; Pred. No. 8.1e-188;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
 QY 8 GCCGAACTCTCTCTCCGTGACAGAGTTATCTCGAGGCTTAATCCACACCGGGA 67
 DB 4 GGAGCCAAAACTCTCTCTGTGACAGAGTTATCTCGAGGCTTAATCCACACCGGGA 63
 QY 68 CTCGAGTCCCGGTTCT 127
 DB 64 CTCGAGTCCCGGTTCT 123
 QY 128 CTCGAGTCCCGGTTCT 187
 DB 124 CTCGAGTCCCGGTTCT 183
 QY 188 CCTTCACT 247
 DB 184 CTTTAACT 243
 QY 248 ATGAGTTTGTCTCAAGAGAAACATTAATTTCTTCAAGAGGTATATGATGATCTTTC 307
 DB 244 ATGAGTTTGTCTCAAGAGAAACATTAATTTCTTCAAGAGGTATATGATGATCTTTC 303
 QY 308 TTCTTTGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 367

Db 304 TTCTTCTGCTCTTTTGTCTGTCTGTGAGTCTTCTGACGATGCGATATGACCGC 363
 Qy 368 TAGGTGGGACATCTGTATACCACTGTGTGTACAGATGACCATGTCCTCCAGGATGTTG 427
 Db 364 TAGGTGGGACATCTGTATACCACTGTGTGTACAGATGACCATGTCCTCCAGGATGTTG 423
 Qy 428 CTCTCTTTTACTGGGTGTCTACGCGAATGCGGGTGTGCGGCTGTGGCTATACAGAAAT 487
 Db 424 CTCTCTTTTGTGGGTGTCTATGCGAATGCGGGTGTGCGGCTGTGGCTATACAGAAAT 483
 Qy 488 ATAGTCTTCTACCTTTTGTGTGACAGACCTTTGTCAATCACTATACATGATGACATCTCT 547
 Db 484 ATATGAACTGACCTCTCTGTGTGTACAACTTTGTCAATCACTATGATGATGATGATCTT 543
 Qy 548 CCCCTTTTGTAGCTCTCTGTGACAAAGGCTTTATCAATTAATGTCGTATCTTTATGTT 607
 Db 544 CCTCTCTGTAGCTCTCTGTGACAAAGGCTTTATCAATTAATGATGATGATGATGATGTTG 603
 Qy 608 GTGACGCTGTGATGCGGGTGTGCGCAATGTCGTGCTTTTATCTTTATGATGATGATGTT 667
 Db 604 GTGCTGTGTGATGCGGGTGTGCGCAATGTCGTGCTTTTATCTTTATGATGATGATGTT 663
 Qy 668 TCCAGCATTCCTCGGCTGTGATGTCGTGTGAGGCGAGGCTTAAAGCTTCACTGACGAC 727
 Db 664 TCCAGCATTCCTCGGCTGTGATGTCGTGTGAGGCGAGGCTTAAAGCTTCACTGACGAC 723
 Qy 728 TCTTACATTAATGAGCTTTCTCTTTCTTTTGTGTGTGAGGAGCTTTTATGATGATGATG 787
 Db 724 TCCACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 783
 Qy 788 CCTTCCATTTTACCTCTGTGACAAAGGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 847
 Db 784 CTTCATCT 843
 Qy 848 CCCATGTTTAAACCTTATATCTACAGCTGTGAGAAATGATGATGATGATGATGATGATG 907
 Db 844 CCCGTTTAAACCTTATATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 903
 Qy 908 AGAACCTTTTCCAGATTAAGCTTTCTCTGA 937
 Db 904 AGAACCTTTTCCAGATTAAGCTTTCTCTGA 933
 RESULT 12
 AAS42233
 ID AAS42233 standard; cDNA; 933 BP.
 AC AAS42233;
 XX
 DT 18-DEC-2001 (first entry)
 DE Human cDNA encoding olfactory receptor AOLFPR26.
 DE
 KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
 KW ss; food additive; cosmetic; fragrance; pharmaceutical additive.
 XX
 OS Homo sapiens.
 PN W0200168805-A2.
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001W0-US007771.
 XX
 PR 13-MAR-2000; 2000US-0188914P.
 PR 24-MAR-2000; 2000US-0192033P.
 PR 12-APR-2000; 2000US-0198474P.
 PR 24-APR-2000; 2000US-0199335P.
 PR 26-MAY-2000; 2000US-0207782P.
 PR 23-JUN-2000; 2000US-0213849P.
 PR 16-AUG-2000; 2000US-0226534P.
 PR 07-SEP-2000; 2000US-0230732P.
 PR 07-FEB-2001; 2001US-0266862P.

XX (SEN0-) SENOMYX INC.
 PA Zozulya S;
 XX WPI; 2001-570867/64.
 DR P-PSDB; AAU24540.
 PT Nucleic acid encoding human olfactory G protein-coupled receptors,
 PT useful for screening for compounds involved in olfactory sensation, where
 PT the compounds can be used in the food, pharmaceutical and cosmetic
 PT industries to customize odors.
 XX
 PS Claim 1; Page 94; 319pp; English.
 CC The invention relates to nucleic acids encoding human olfactory
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's
 CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence encodes a human olfactory receptor of
 CC the invention
 CC
 SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
 Query Match 71.8%; Score 691.6; DB 5; Length 933;
 Best Local Similarity 84.0%; Pred. No. 8.1e-188;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
 Qy 8 GCGGAACT 67
 Db 4 GCGGAACT 63
 Qy 68 CTCGAGTCT 127
 Db 64 CTCGAGTCT 123
 Qy 128 CTGGGCTTATATCT 187
 Db 124 CTGGGCTTATATCT 183
 Qy 188 CCTTCAACTGCT 247
 Db 184 CCTTCAACTGCT 243
 Qy 248 ATGAGTTTGTCTCAAGGAAGACATTTTCT 307
 Db 244 ATGAGTTTGTCTCAAGGAAGACATTTTCT 303
 Qy 308 TTTCT 367
 Db 304 TTTCT 363
 Qy 368 TACGTGGGACATCTGTAAACCACTGTGTACACATGATGATGATGATGATGATGATGATGATG 427
 Db 364 TACGTGGGACATCTGTAAACCACTGTGTACACATGATGATGATGATGATGATGATGATGATG 423
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 Db 544 CCTCTCTGTAGCTCTCTGTGACAAAGGCTTTATCAATTAATGTCGTATGATGATGATGATGATG 603

QY 608 GTGACCGTTGGCATTTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATTCTT 667
 DB 604 GTGGCTGTGAGCTTGGATGAGTCCCATGTCACCTCTTTATTTCTTATGCTTCACTC 663
 QY 668 TCCAGCATTTCCGGCTTATGTTCTGCTGAGGCGAGTCTTAAGCCTTCACTAGCTCAGC 727
 DB 664 TCCAGCATTTCAACACAGTCTTACAGAGGCGAGTCCAAAGCCTTATGTACTTCAAGT 723
 QY 728 TCCATCAATATGAGTCTCTCTTTCTTTGGGTCAGAGAGCTTTAGTCTCCCAACCC 787
 DB 724 TCCACATTAATTTAGTCTCTCTTTCTTTGGTCTGCTCTTCAATGCTCAACCC 783
 QY 788 CTTTCATATTTTACCCCTGAGACAGGAGAAAGTCTCTCTGTTCTTATACACTGTGTG 847
 DB 784 CTTTCATATCTGCCCCCTGAGCAAGGAAAGTCTCTCTGTTCTTATACATAATAGTC 843
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 DB 844 CCGGTTTAAACCATTAATCTATAGCTTGAAGAACAGAGATGCAAGTGTGCTGAG 903
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 DB 904 AGAAGCTTTGGGAGAAATCTTTCTTAA 933

RESULT 13
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 ID ABZ43067 standard; DNA; 933 BP.
 XX ABZ43067;
 AC 06-VAR-2003 (first entry)
 DT 06-VAR-2003 (first entry)
 XX 06-VAR-2003 (first entry)
 DE Human GPCR polynucleotide SEQ ID NO 395.
 XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;
 KM drug development; gustatory; taste; fragrance; gene; ds.
 KM Homo sapiens.
 OS Homo sapiens.
 PN WO200216548-A2.
 XX 28-FEB-2002.
 XX 30-JUL-2001; 2001WO-1B001446.
 XX 04-AUG-2000; 2000JP-00237818.
 PR 13-FEB-2001; 2001JP-00034434.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Haga T, Takeda S, Mitaku S;
 PI WPI; 2002-304118/34.
 DR P-Psdb; ABP95793.
 XX Database global search for G protein-coupled receptors, proteins and
 PT encoded genes for studying in vivo signal transduction mechanism and
 PT identifying targets for drug development.
 XX Claim 9; SEQ ID NO 395; 97bp + Sequence Listing; Japanese.

The invention relates to a method for screening G protein-coupled
 CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins (ABP95596-
 CC ABP95962) by extracting open-reading frames containing 6-8 transmembrane
 CC domains with 250-1000 amino acid residues to give a gene homologous with
 CC a known GPCR gene. The receptor proteins and encoded genes are useful for
 CC studying in vivo signal transduction mechanism and identifying targets
 CC for drug development e.g. based on olfactory and gustatory receptors in
 CC form of agonists and antagonists by screening intrinsic and extrinsic
 CC ligands as bitter taste inhibitors, taste enhancers and fragrance
 CC improvers. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly

CC from WIP0 at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;
 Query Match 71.8%; Score 691.6; DB 6; Length 933;
 Best Local Similarity 84.0%; Pred. No. 8.1e-188;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 8 GCGAGAGACCTCCCTCCGAGAGAGTATCTCTGAGGAGCTTATCCAGACAGCGGGA 67
 DB 4 GCAGCCAAAACCTTTCTGTGACAGAGTTATCTCGAAGCTTAAACCCAGCGGGA 63
 QY 68 CTCAGAGTCCCGCT 127
 DB 64 CTCAGAGTCCCGCT 123
 QY 128 CTCAGAGTCCCGCT 187
 DB 124 CTCAGAGTCCCGCT 183
 QY 188 CCGTTCACCTGCTCCCT 247
 DB 184 CTTTTCACCTGCTCCCT 243
 QY 248 ATGAGTCTTGTCTCAAGAGAAATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 307
 DB 244 ATGAGTCTTGTCTCAAGAGAAATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 303
 QY 308 TTTCTCTGTTCT 367
 DB 304 TTTCTCTGTTCT 363
 QY 368 TACGTGGCATCTGTATCCCAAGCTGTATACAGATACCAATGCTCTCCAGAGTGTG 427
 DB 364 TACGTGGCATCTGTATCCCAAGCTGTATACAGATACCAATGCTCTCCAGAGTGTG 423
 QY 428 CTCCTTTTACCTGAGTGTCTCAAGAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGT 487
 DB 424 CTCCTTTTACCTGAGTGTCTCAAGAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGT 483
 QY 488 ATAGTGTCTCTCACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 547
 DB 484 ATAGTGTCTCTCACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 543
 QY 548 CCGCTCTTGAAGTCTCTCTCTCAAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGT 607
 DB 544 CCGCTCTTGAAGTCTCTCTCTCAAGAGGAGGAGTGTGTGTGTGTGTGTGTGTGT 603
 QY 608 GTGACCGTTGGCATTTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATTCTT 667
 DB 604 GTGACCGTTGGCATTTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATTCTT 663
 QY 668 TCCAGCATTTCCGGCTTATGTTCTGCTGAGGCGAGTCTTAAGCCTTCACTAGCTCAGC 727
 DB 664 TCCAGCATTTCAACACAGTCTTACAGAGGCGAGTCCAAAGCCTTATGTACTTCAAGT 723
 QY 728 TCCATCAATATGAGTCTCTCTTTCTTTGGGTCAGAGAGCTTTAGTCTCCCAACCC 787
 DB 724 TCCACATTAATTTAGTCTCTCTTTCTTTGGTCTGCTCTTCAATGCTCAACCC 783
 QY 788 CTTTCATATTTTACCCCTGAGACAGGAGAAAGTCTCTCTGTTCTTATACACTGTGTG 847
 DB 784 CTTTCATATCTGCCCCCTGAGCAAGGAAAGTCTCTCTGTTCTTATACATAATAGTC 843
 QY 848 CCGATGTTTAAACCATTAATCTAGAGCTGAGAAATAGGATGCAACTGCTGCTGAG 907
 DB 844 CCGGTTTAAACCATTAATCTATAGCTTGAAGAACAGAGATGCAAGTGTGCTGAG 903
 QY 908 AGAACCTTTTCCAGAAATAGCTTTTCTTGA 937
 DB 904 AGAAGCTTTGGGAGAAATCTTTCTTAA 933

RESULT 14
ABK68455
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XX
AC ABK68455;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human DNA for olfactory and pheromone G protein-coupled receptor #55.
XX
KW Human; de; gene; olfactory and pheromone G protein coupled receptor;
KW GPCR; tranquilizer; antidepressant; neuroleptic; endocrine; anabolic;
KW anorectic; taste; fragrance; food additive; cosmetic; cell migration;
KW sterility; psychotic disorder; neurological disorder; anxiety;
KW schizophrenia; manic depression; depression; axonal growth;
KW menstrual cycle; appetite sexual motivation; sexual attraction;
KW aggression.
XX
OS Homo sapiens.
XX
PN W0200224726-A2.
XX
PD 28-MAR-2002.
XX
PE 21-SEP-2001; 2001MO-BE000162.
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PR 22-SEP-2000; 2000EP-00870211.
XX
PA (CHEM-) CHEMCOM SA.
XX
PI Velthen A;
XX
DR WPI: 2002-330013/36.
DR P-PSDB; AAU95568.
XX
PT Novel pheromone G-protein coupled receptor and receptor-derived agonists,
PT antagonists or inhibitors useful in food or cosmetic products or in the
PT treatment or prevention of neurological disorders such as anxiety and
PT schizophrenia.
XX
PS Disclosure; Page 178-179; 833pp; English.
XX
CC The invention relates to olfactory and Pheromone G-protein coupled
CC receptor (GPCR) or a protein 95% identical to the GPCR, a specific active
CC portion and its encoding polynucleotide. Also included are an agonist,
CC antagonist or inhibitor of the GPCR or the polynucleotide, a vector
CC comprising the polynucleotide, a cell transformed by the vector, a non-
CC human mammal comprising a partial or total deletion of the polynucleotide
CC encoding the receptor and screening (detection and possibly, recovering)
CC of compounds which are known or not known to be agonist, antagonists or
CC inhibitors of natural compounds to the GPCR. The receptor-derived
CC agonists, antagonists, inhibitors or compounds are used as an
CC improvement, elimination or substitution of an existing taste and/or a
CC fragrance of (or in) the food and/or cosmetic products. They can also be
CC used in the preparation of medicament in the treatment and/or prevention
CC of a mammalian disorder, such as cell migration, sterility, psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, depression, for promoting axonal growth, nerve cell
CC connection and nerve regeneration for modulating male and female
CC endocrine functions, hormone production and the menstrual cycle, for the
CC prevention of the treatment by stimulation of several mammalian
CC behaviours, such as stimulation or suppression of appetite, sexual
CC motivation, sexual attraction, aggression and for promoting or
CC suppressing chemical communication between organisms. The present
CC sequence is a human DNA encoding an olfactory and pheromone GPCR
XX
SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;

Query Match 71.8%; Score 691.6; DB 6; Length 933;
Best Local Similarity 84.0%; Pred. No. 8.1e-188;
Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

GY 8 GCCGAGACCTCCCTCCGTCAGACAGATTATCTCCGACGAGTTATCTACACACCGCGGA 67

DB 4 GCAGCCAAAACCTCTCTGTGACAGAGTTTCTCTCGAAGGCTTAACCCACGCGCGGA 63
|||
QY 68 CTCACAGTCCCGCTCTTCTCTCTTTTACGTTTCAACGGCTCAAGGTGGGGAAC 127
|||
DB 64 CTGCGATCCCGCTCTTCTCTCTTTCTGAGTTTCAACGGCTCAAGGTGGGGAAC 123
|||
QY 128 CTGGGCTTGAATATCTGATAGAGGCTCAACTCTGCGCTGATATCCCATGATCTTTTC 187
|||
DB 124 CTGGGCTTGAATATCTGATAGAGGCTCAACTCTGCGCTGATATCCCATGATCTTTTC 183
|||
QY 188 CCTTCACTGTTGCTCTGATATTTTATTTTCTCTACAGCATCATCTCCCAAAATCTG 247
|||
DB 184 CTTTAACTCTCTTATATGATTTCTGTTTCTCACTACACATCTCCCAAAATCTG 243
|||
QY 248 ATGAGTTTGTCTCAGAGAGACATTAATTTCTTCAAGGTTATAGTCACTTTTC 307
|||
DB 244 ATGAGTTTGTCTCAGAGAGACATTAATTTCTTCAAGGTTATAGTCACTTTTC 303
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QY 308 TTTCTCTGTTTCTTCTCTTCTTCTGAGTCTTCACTCTGCGGAGATGTGAGAGACCC 367
|||
DB 304 TTTCTCTGTTTCTTCTCTTCTTCTGAGTCTTCACTCTGCGGAGATGTGAGAGACCC 363
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QY 368 TACGTGGGATCTGTAACCCACTGTTTGAACAGATCAACATGTCCTCCAGGTGTGTTG 427
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DB 364 TACGTGGGATCTGTAACCCACTGTTTGAACAGATCAACATGTCCTCCAGGTGTGTTG 423
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QY 428 CTCCTTTTACGTGTTCTACAGGATGGGGTTTGGGGCTGTGGCTATACAGAAAT 487
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QY 488 ATAGTGTTCCTACCTTTTGTGACAGACACACTTGTCAATCACTACATGTGACATCTT 547
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DB 484 ATAGTGTTCCTACCTTTTGTGACAGACACACTTGTCAATCACTACATGTGACATCTT 543
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DB 544 CCCCTTTTACCTTCTCTGACAGGCTCTTACATTAATGCTCTGTGATCTTATTTGTT 603
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DB 604 GTGACCGTTGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 663
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QY 728 TCCATCATATGAGGCTTCTCTTCTTCTTGGGTCAAGAGCTTTAAGTCACTCAACC 787
|||
DB 724 TCCATCATATGAGGCTTCTCTTCTTCTTGGGTCAAGAGCTTTAAGTCACTCAACC 783
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QY 788 CCTTCATTTTACCTCTGAGACAGGGAAGTGTCTCTCTGTTCTTACACGTGTGTTG 847
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DB 784 CCTTCATTTTACCTCTGAGACAGGGAAGTGTCTCTCTGTTCTTACACGTGTGTTG 843
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QY 848 CCCATGTTTAAACCATTTATCTTACAGCTGAGAAATAGATGCAAACTTGGCTGAAG 907
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DB 844 CCCATGTTTAAACCATTTATCTTATAGCTTGAGAAACAAAGATGCAAAAGTTGCCGTGAG 903
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QY 908 ABAACCTTTTCCAGATATAGCTTTTCTGA 937
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DB 904 ABAACCTTTTCCAGATATATCTTTCTTAA 933
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RESULT 15
ABK37521
ID ABK37521 standard; cDNA; 933 BP.
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AC ABK37521;
XX
DT 08-MAY-2002 (first entry)
XX
DE DNA encoding G-coupled olfactory receptor #23.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2004, 22:46:01; Search time 4162 Seconds
(without alignment)

10028.674 Million cell updates/sec

Title: US-10-023-597-23

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Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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31: em_htg_inv:*
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	961.4	99.8	192926	9	AP000916 Homo sapi
4	960.4	99.7	994	6	AX241500 Sequence
5	755.4	78.4	931	6	AX646877 Sequence
6	751	78.0	935	6	AX241493 Sequence
7	694.2	72.1	991	6	AX702842 Sequence
8	694.2	72.1	1333	6	AX646099 Sequence
9	694.2	72.1	1333	9	AB065834 Homo sapi
10	694.2	72.1	150847	9	AP001524 Homo sapi
11	694.2	72.0	172991	2	AC083958 Homo sapi
12	693	72.0	976	6	AX583206 Sequence
13	692.4	71.9	953	6	AX554459 Sequence
14	691.6	71.8	933	6	AX244609 Sequence
15	691.6	71.8	933	6	AX244843 Sequence
16	691.6	71.8	933	6	BD144473 Novel G-P
17	690.2	71.7	930	6	AX242246 Sequence
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19	663.2	68.7	258873	2	AC096935
20	657.6	68.3	936	10	AY073678
21	657.6	68.3	936	10	AY318059 Mus muscu
22	657.4	68.3	989	6	AX702946 Sequence
23	657.4	68.3	1336	6	AX646461 Sequence
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25	657.4	68.0	1655	6	AX357037 Sequence
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32	647.2	66.6	933	6	AX242071 Sequence
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35	612.6	63.6	667	9	AX448759 Cercopit
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45	594.4	61.7	209644	10	AC074314

ALIGNMENTS

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LOCUS AX555964 963 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 23 from Patent WO0250275.
ACCESSION AX555964
VERSION AX555964.1 GI:25899399
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Padigaru,M., Kekuda,R., Li,J., Ballinger,R.A., Casman,S.J.,
Spytek,K.A., Baumgartner,J.C. and Burgess,C.E.
TITLE Novel proteins and nucleic acids encoding same

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Query Match	99.8%	Score 961.4;	DB 2;	Length 172991;
Best Local Similarity	99.9%	Pred. No. 2.8e-233;		
Matches 962; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	AATGGCTCCGAGAACTCTCTCCGTGACAGAGATTATCTCGACGGCTTAATCCACCA	60
Db	94317	AATGGCTCGGAGAACTCTCTCCGTGACAGAGATTATCTCGACGGCTTAATCCACCA	94378
QY	61	GCCGGGATCTCAGGTCCCGCTTCTTCTCTGTTCTATGAGTTCTAAGCGGTCAACGGTGGT	120
Db	94377	GCCGGGATCTCAGGTCCCGCTTCTTCTCTGTTCTTAGTTCTACACGGGTCAACGGTGGT	94438
QY	121	GGGGAACCTGGGCTGTGATATCTGATAGAGGCTCACTCTGGCTGTCATATCCCATGTG	180
Db	94437	GGGGAACCTGGGCTGTGATATCTGATAGAGGCTCACTCTGGCTGTCATATCCCATGTG	94498
QY	181	CTTTTTCCTCCCACTGTCCCTCGTGGATTTAGTTCTCTCAAGCAATCAATCCCA	240
Db	94497	CTTTTTCCTCCCACTGTCCCTCGTGGATTTAGTTCTCTCAAGCAATCAATCCCA	94558
QY	241	AATGTGATGAGTTTGTCTCAGGAGACATTAATTTCTTACAGGAGTATGAGTCA	300

Db	94557	AAATGCTGATGATTTTGTCTCAGAGAAACATTAATTTCTTTCACAGGATGATAGCTA	94616
QY	301	GTCTCTCTCTCTCTGTTCTTTCTTTGCTTTTCTGAGTCTTCACTCTGTGGAGATGATGCA	360
Db	94617	GTCTCTCTCTCTCTGTTCTTTCTTTGCTTTTCTGAGTCTTCACTCTGTGGAGATGATGCA	94678
QY	361	GGACCGCTAGCTGGGCACTGTACAACCACTGTGTACAAGATACCAATGTCTCCGAGG	420
Db	94678	GGACCGCTAGCTGGGCACTGTACAACCACTGTGTACAAGATACCAATGTCTCCGAGG	94733
QY	421	GTGTTTCTCTCTTTTACTGAGGATCTACGGAGTGGGGGTTTTTGGGGCTGTGTGCTATAC	480
Db	94737	GTGTTTCTCTCTTTTACTGAGGATCTACGGAGTGGGGGTTTTTGGGGCTGTGTGCTATAC	94793
QY	481	AGGAATATATGTTTCTCACCTTTTGTGAGACAACTTGTCAATCACTACATGTGTGA	540
Db	94797	AGGAATATATGTTTCTCACCTTTTGTGAGACAACTTGTCAATCACTACATGTGTGA	94853
QY	541	CATCTCTCCCTCTTGTAGCTCTCTGCAACGGCTCTTACATTAATGTCTGTGATCTT	600
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QY	601	TATGTTGTGACCGTGGCATTTGGGGTGGCCATTTGTCGGCTTTTATCTCTATAGTTT	660
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QY	661	TATCTCTTCAAGCATTTCTCGCGCTTATCTTGCTGAGGGGAGGCTTAAACCTTCACTAG	720
Db	94977	TATCTCTTCAAGCATTTCTCGCGCTTATCTTGCTGAGGGGAGGCTTAAACCTTCACTAG	95033
QY	721	CTGAGCTCTTCACTAAATGCAATTTCTCTTTTCTTGGTCAAGAGCTTTTACGTACT	780
Db	95037	CTGAGCTCTTCACTAAATGCAATTTCTCTTTTCTTGGTCAAGAGCTTTTACGTACT	95093
QY	781	CAAAACCCCTTCCATTTTACCCCTGGACCAAGGGGAAGTCTCCCTCTCTATATACAC	840
Db	95097	CAAAACCCCTTCCATTTTACCCCTGGACCAAGGGGAAGTCTCCCTCTCTATATACAC	95153
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Db	95157	TGTGTGGCCATGTTTAAACCATTAATCTACAGCTCAGGAATTAAGGATGTCAAACCTTGC	95213
QY	901	CTGGAAGGAACCTTTTCCAGAATTAAGCTTTTCTTGAAAAAATTTTAGAAACAGAAAG	960
Db	95217	CTGGAAGGAACCTTTTCCAGAATTAAGCTTTTCTTGAAAAAATTTTAGAAACAGAAAG	95273
QY	961	AGA 963	
Db	95277	AGA 95279	

[illegible]

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matches 1; indels 0; gaps 0;
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ACCAGGGGAAGTGTCTCCTCCTGTTCTATAC

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1; Indels 0; Gaps 0;
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GGTTTGGGCTGTGCTCATCA 481

ORIGIN	Query Match	78.4%;	Score 755.4;	DB 6;	Length 931;
	Beet Local Similarity	99.9%;	Pred. No. 4.5e-151;		
	Matches 756;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	207 TAGATTTAGTTTCTCTACGACCATCATCTCCCAAAATGCTGATGAGTTTGTCTCAAGA				266
Db	1 TAGATTTAGTTTCTCTACGACCATCATCTCCCAAAATGCTGATGAGTTTGTCTCAAGA				60
Qy	267 AGAACATTATTTCTTCTACAGGGGTGTAAGATCAGTTCTTCTTCTGTCTTTGTGCT				326
Db	61 AGAACATTATTTCTTCTACAGGGGTGTAAGATCAGTTCTTCTTCTGTCTTTGTGCT				120
Qy	327 TTTCTGAGTCCTTATCCTGTGCGCGAATGGTGGAGAACCGCTACGTGGAGCATCTGTAAC				386
Db	121 TTTCTGAGTCCTTATCCTGTGCGCGAATGGTGGAGAACCGCTACGTGGAGCATCTGTAAC				180
Qy	387 CACTGTGTACAGCATGACCATGTCTCCCAAGTGTGTGCTCTCTTTTACTGCGTGTCT				446
Db	181 CACTGTGTACAGCATGACCATGTCTCCCAAGTGTGTGCTCTCTTTTACTGCGTGTCT				240
Qy	447 ACGGATGGGGGCTTTTGGGGCTGTGGCTCAACAGGAAATATAGTGTCTCACCTTT				506
Db	241 ACGGATGGGGGCTTTTGGGGCTGTGGCTCAACAGGAAATATAGTGTCTCACCTTT				300
Qy	507 GTGAGACAAACCTTGTCAATCACTACATATGTGTGATCTCTTCCCTTTGAGCTCTCT				566
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Qy	567 GCAAGCGCTCTTAATAATATCTCTGTGCATCTTTATGTGTGTACCGTGGCAATGGGG				626
Db	361 GCAAGCGCTCTTAATAATATCTCTGTGCATCTTTATGTGTGTACCGTGGCAATGGGG				420
Qy	627 TGCCATGTGTGCGGTTTATCTCTTAATGTTTTATCTTTCCAGCATCTCCGCGTTA				686
Db	421 TGCCATGTGTGCGGTTTATCTCTTAATGTTTTATCTTTCCAGCATCTCCGCGTTA				480
Qy	687 GTTCTGTGAGGGGAGCTTAAGCCTTCAGTACGTGACGTCTCTACATAATTGCAGTTT				746
Db	481 GTTCTGTGAGGGGAGCTTAAGCCTTCAGTACGTGACGTCTCTACATAATTGCAGTTT				540
Qy	747 CTCTTTCTTTGGGTGAGGAGCTTTTACGTACCTCAACCCCTCCATTTTACCCCTGG				806
Db	541 CTCTTTCTTTGGGTGAGGAGCTTTTACGTACCTCAACCCCTCCATTTTACCCCTGG				600
Qy	807 ACCAGGGGAAAGTGTCTCTCCTGTCTTATACACACTGTGTGCCCATGTTAACCCATTAA				866
Db	601 ACCAGGGGAAAGTGTCTCTCCTGTCTTATACACACTGTGTGCCCATGTTAACCCATTAA				660
Qy	867 TCTACAGCTGAGGAATTAAGATGTGCAAACTTGCCTGGAAGAAGACCTTTCCAGATTA				926
Db	661 TCTACAGCTGAGGAATTAAGATGTGCAAACTTGCCTGGAAGAAGACCTTTCCAGATTA				720
Qy	927 GCTTTTCTGAAAAAATTTTGAAGAACGAAAGAGA 963				
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RESULT 6	AX241493	935 bp	DNA	linear	PAT 26-SEP-2001
LOCUS	Sequence 241 from Patent WO0127158.				
DEFINITION	AX241493				
ACCESSION	AX241493.1				
VERSION	GI:15798368				
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
REFERENCE	synthetic construct				
AUTHORS	artificial sequences.				
TITLE	1 Bellenson, J., Smith, D., Lancet, D., Glusman, G., Fuchs, T. and Yanai, I.				
	Olfactory receptor sequences				

QY 548 CCCCTTCTTGTAGCTCTCTGTGCAAGGCGCTTACATTAATGTCCTGATCTTTATGTT 607
DB 592 CCTCTCCTTGTAGCTCTCTGTGCAAGGCGCTTACATTAATGTCCTGATCTTTATGTTG 651
QY 608 GTGACCGTGTGAGTGGGGGTGCGCATTTGTCGCTTTTATCTTATGTTATGTTCTT 667
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QY 668 TCCAGCATTTCTCCGCTTATGTTCTGCTGAGGCGAGCTTAAAGCCTTCACTGACG 727
DB 712 TCCAGATTTCTACAGAGGCTTCTACAGAGGCGAGCTTAAAGCCTTCACTGACG 771
QY 728 TCTCATATATGTGAGTCTTCTTTCTTTGGGTGAGAGCTTTACAGTCTTCAAAACC 787
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DB 832 CTTTCATCTCTCCCTGTGACGAGGAGGAGTCTCTCCCTGTTCTATACACTATAGTC 891
QY 848 CCCATGTTTAACTCCATTAATCTACAGCTGAGAGATTAAGATGTCAACTTCCCTGAG 907
DB 892 CCCGTTTAACTCCATTAATCTATAGCTTGAAGAACAGAGATGTCAAGTGTCCCTGAGG 951
QY 908 AGAACCTTTTCCAGATTAAGCTTTCTTGAATAAAATTT 946
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RESULT 8
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LOCUS
DEFINITION
Sequence 291 from Patent EP1270724.
AX646099
VERSION
AX646099.1 GI:28798478
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
Suwa, M., Asei, K., Akiyama, Y. and Aburatani, H.
TITLE
Guanine triphosphate-binding protein coupled receptors
JOURNAL
Patent: EP 1270724-A 291 02-JAN-2003;
National Institute of Advanced Science and Technology Incubation, Ltd.
(JP) ; Center for Advanced Science and Technology Incubation, Ltd.
(JP)

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Location/Qualifiers
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CDS
Query Match 72.1%; Score 694.2; DB 6; Length 1333;
Best Local Similarity 83.7%; Pred. No. 1,7e-165;
Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

ORIGIN
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DB 264 CTGGAGATCCCGCTCTTCTCTCTGTTCTAGTTTCTACGCGGTCACGGTGAGGGAAC 323
QY 128 CTGGGCTTATATCCGATAGGAGCTCACTCTGCTGATATGCCCATGATCTTTTC 187
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QY 188 CCTCTCACTTGTCCCTGTGATATTTAGTTTCTTACAGACCATCATTTCCCAAAATGCTG 247
DB 384 CTTTATACCTCTCTTATATGATTTCTGTTTCTTCACTACATCACTCCCAAAATGCTG 443
QY 248 ATGAGTTTGTCTCAAGAGAACATTTATCTCTACAGGAGTATGATCAGTTCTTC 307
DB 444 ATGAGTTTGTCTCAAGAGAACATTTATCTCTACAGGAGTATGATCAGTTCTTC 503
QY 308 TTTCTCTGTTCTTTGTTCTTTCTGAGTCTTCACTCTGCTGAGATGTGAGAGACCC 367
DB 504 TTTCTCTGTTCTTTGTTCTTTCTGAGTCTTCACTCTGCTGAGATGTGAGAGACCC 563
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DB 564 TACGTGGGCACTGTGATACCCAGCTGTTGATACAGTACCATGTCCTCCAGAGTGTGTTG 623
QY 428 CTCTTTTACTGAGGTGTCTACGAGGATGGGGATTTTGGGGCTGTGCTCATPACAGGAAT 487
DB 624 CTCTTTTACTGAGGTGTCTACGAGGATGGGGATTTTGGGGCTGTGCTCATPACAGGAAT 683
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DB 684 ATAGTGTCTTCTACCTTTTGTGACAGACACTTGTCAATACATCATGTGTGATCTCT 743
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DB 864 TCCGAGATCTCCGCGTATGTTCTGAGGCGAGTCTAAAGGCTCAGTACGTGAGC 923
QY 728 TCTCATATATGAGTGTCTCTTTCTTTGGGTGAGAGCTTTTACGATCTCAAAACC 787
DB 924 TCCCATATATGATGTTCTCTTTCTTTGGGTGAGAGCTTTTACGATCTCAAAACC 983
QY 788 CTTTCATTTTACCCCTGTGACAGGAGGAGTGTCCCTGTTCTATACACTGTG 847
DB 984 CTTTCATTTTACCCCTGTGACAGGAGGAGTGTCCCTGTTCTATACACTGTG 1043
QY 848 CCCATGTTTACCATTAATCTACAGCTGTGAGATTAAGATGTCAAACTTCCCTGAG 907
DB 1044 CCCGTTTAACTCCATTAATCTATAGCTTGTGAGAACAGATGTCAAACTTCCCTGAG 1103
QY 908 AGAACCTTTTCCAGATTAAGCTTTCTTGAATAAAATTT 946
DB 1104 AGAACCTTTGGGCAAAAAATCTTTCTTGAATAAGATTT 1142

RESULT 9
AB065834 1333 bp DNA linear PRI 23-JUN-2002
LOCUS
DEFINITION
Homo sapiens gene for seven transmembrane helix receptor, complete
cde, isolate:CBRC7TM_397.
AB065834
ACCESSION
AB065834.1 GI:21928933
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Suwa, M., Sato, T., Okouchi, I., Arita, M., Futami, K., Matsunoto, S.,
Tsubumi, S., Aburatani, H., Asai, K. and Akiyama, Y.
Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
Unpublished
2 (bases 1 to 1333)
Suwa, M.

Direct Submission
Submitted (11-JUN-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST), 2-41-6 Aomi Koto-Ku, Tokyo 135-0064, Japan
(E-mail: m-suwa@aist.go.jp, URL: http://www.cbrc.jp/
Tel: 81-3-3599-8080, Fax: 81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding (GeneDecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.
And the sequence is submitted by the collaborative project between
[Computational Biology Research Center (CBRC), National Institute
of Advanced Industrial Science and Technology (AIST)] and [Genome
Science Division, Research Center for Advanced Science and
Technology (RCAST), University of Tokyo].

FEATURES

source

Location/Qualifiers
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CDS

ORIGIN

Query Match 72.1%; Score 694.2; DB: 9; Length 1333;
Best Local Similarity 83.7%; Freq. No. 1.7e-165;
Matches 786; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

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204 GCAGCAAAACTCTCTGACAGAGTTATCTCGAGGCTTAATCCACGACCGGGA 263
68 CTCAGAGTCCCGCTCTTCTCTGAGTTTCTACGGGCTACGGTGGGGAAC 127
264 CTGGGAGTCCCGCTCTTCTCTGAGTTTCTACGGGCTACGGTGGGGAAC 323
128 CTGGGCTGATATCTGATAGGGGTCACTCTCGCGGATATCCCATGATCTTTTC 187
324 CTGGGCTGATATCTGATAGGGGTCACTCTCGCGGATATCCCATGATCTTTTC 383
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384 CTTTAAACCTCTTAAATGATTTCTGTTTCTCCACTCAATCACTCCCAAAATGCTG 443
248 ATGAGTTTCTGATAGGAGAAATATTTCTCTACGAGGCTATAGATCTGCTTC 307
444 ATGAGTTTCTGATAGGAGAAATATTTCTCTACGAGGCTATAGATCTGCTTC 503
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QY 368 TAGGGGACATCTGTAAACCACTGTTGTACAGATACCAATGTCCTCCAGGNGTTTG 427
DB 564 TAGGGGACATCTGTAAACCACTGTTGTACAGATACCAATGTCCTCCAGGNGTTTG 623
QY 428 CTCCTTTTACTGGGATGTCTACGGGATGGGGGTTTTTGGGCTGTGCTCATACAGAAAT 487
DB 624 CTCCTTTTGTGGGTGTATGGGATGGGGTGTGCTGGGGCCATGGCCACAGAGAAC 683
QY 488 ATAGTGTCTACCTTTTGTGAGAACACCTTGTATACATCACTACATGTGTACATCTT 547
DB 684 ATAGTGTCTACCTTTTGTGAGAACACCTTGTATACATCACTACATGTGTACATCTT 743
QY 548 CCCCTTTTGGAGCTCTCTGCAACGAGCTTACATTAATGTCTGTCATCTTTATTTGT 607
DB 744 CTCCTCTTGGAGCTCTCTGCAACGAGCTTACATTAATGTCTGTCATCTTTATTTGT 803
QY 608 GTACCGCTTGGAGCTTGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGAT 667
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QY 668 TCAGCATCTCCGCTGTAGTTCTGTGAGGAGGCTTAAGCCTTGATAGCTGAGC 727
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QY 788 CCTTCATTTTCCCTGACAGAGGAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 847
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QY 848 CCCATGTTTAAACCATTAATCTACAGCTGAGAGATTAAGATGCAATCTGCTGAG 907
DB 1044 CCCGTTTAAACCATTAATCTATGCTTGAAGAACAGAGATGCAATGCTGAGG 1103
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DB 1104 AGAAGCTTTCCAGAAATAGCTTTCTTGAATAAATTT 1142

RESULT 10
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LOCUS
DEFINITION
AP001524 Homo sapiens genomic DNA, chromosome 11q, clone:RP11-702P11,
complete sequence.
ACCESSION
AP001524
VERSION
AP001524.4 GI:15320470
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens genomic DNA
Published Only in Database (2000)
2 (bases 1 to 150847)
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (22-MAR-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@sc.riken.go.jp, URL: http://hgp.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
On Aug 27, 2001 this sequence version replaced gi:9798616.
COMMENT
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RESULT 13					
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LOCUS	AX554459				
DEFINITION	Sequence 13 from Patent WO0246229.				
ACCESSION	AX554459				
VERSION	AX554459.1				
KEYWORDS	GI:25898221				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				

Query Match	71.9%	Score 692.4;	DB 6;	Length 953;
Best Local Similarity	83.8%	Pred. No. 4.7e-165;		
Matches 783; Conservative	0;	Mismatches 151;	Indels 0;	Gaps 0

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QY	128	CTGGGCTTGATATCTGTATAGAGGCTCAACTCTCGCGTCGATATCCCATGTACTTTTC	187
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QY	188	CCCTTCAACTGTCCCTCGTAGATTTTAGTTTCTCTACGACCATCATTTCCAAATGCTG	247
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 LOCUS Sequence 35 from Patent WO0166742.
 DEFINITION AX244609
 ACCESSION AX244609
 VERSION AX244609.1 GI:15859510
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Lal, P., Tang, Y.T., Patterson, C., Yao, M.G., Shih, J.L.,
 Tribouley, C.M., Lu, D.A., Yue, H., Khan, F.A., Policky, D.L.,
 Au-Yang, J., Yang, J., Harland, L., Walsh, R.T., Lo, T.P. and
 Borowsky, M.L.
 G-protein coupled receptors
 Patent: WO 0166742-A 35 13-SEP-2001;
 Incyte Genomics, Inc. (US)
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 Best Local Similarity 84.0%; Pred. No. 7,66-165;
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 QY 8 GCGGGAAGTCTCTCTCGTGAAGAGTTTATCTCGAGGCTTAATCCACCGCGGA 67
 Db 4 GAGGCCAAAACCTCTCTGTGACAGAGTTTATCTCGAGGCTTAATCCACCGCGGA 63
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 Db 64 CTGCGGATCCCGCTCTCTCTGTGAGTTTCTAAGGCTGACGGGTGAGGGGAGAC 123
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 QY 308 TTTCTTGTCTTCTTGTCTTTTGTAGTCTCTAATCTGCGGAGAGTGTGAGACCG 367
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 AX448443 933 bp DNA linear PAT 03-JUL-2002
 LOCUS Sequence 109 from Patent WO0224726.
 DEFINITION AX448443
 ACCESSION AX448443
 VERSION AX448443.1 GI:21697342
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Velken, A.
 Olfactory and pheromones g-protein coupled receptors
 Patent: WO 0224726-A 109 28-MAR-2002;
 ChemCom S.A. (BE)
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 /note="unnamed protein product"
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 /db_xref="GI:21697343"
 /db_xref="EMBL:CAD37543"
 /translation="MAKNSVTEFFIBGLTHPGRLRPLFLELFGYVTVVGNIGL
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 FCFEVSSEFSLSAAYDRVAICNPILYTVMSQVCLILLGAYGAGFAAHTG
 SIMLITFCADNLVNHFMCDLPLLELSCNSYMEILVVFIVADVCMPIVTVIVISA
 LILSLIHSSTERSKAFSTCSHIIIVSLFPGSAFVILKPLSLILPBGKXVSLF
 YTIIVPVLNPIYSLRKDVVALRRLGRKIFS"
 ORIGIN
 Query Match 71.8%; Score 691.6; DB 6; Length 933;
 Best Local Similarity 84.0%; Pred. No. 7,66-165;
 Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
 QY 8 GCGGGAAGTCTCTCTCGTGAAGAGTTTATCTCGAGGCTTAATCCACCGCGGA 67

Thu Sep 30 08:53:36 2004

us-10-023-597-23.rge

Page 13

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Db      124 CTGGGCTTGATATACCTGATGGGCTGAATCTACCTGCACACTCCCATGACTTCTTC 183
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Db      244 ATGAGTTTGTCTCAGAGAAACATTAATTTCTTCCACAGGTTGATAGTCTTC 303
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QY      428 CTCCTTTTACTGGGTGTCTACAGGGAATGGGGTTTGGGGCTGTGGCTATACAGGAAT 487
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Db      664 TCCAGCATTCCTCGGCTAGTCTGTGCTGAGGCGAGTCTAAAGCCTTCACTGAGTGCAGT 723
QY      728 TCCCTCATATATGCAAGTCTCTTCTTGTGGTCAAGAGCTTTAGCTTAACCTCAAAACC 787
Db      724 TCCCTCATATATATGCAAGTCTCTTCTTGTGGTCAAGAGCTTTAGCTTAACCTCAAAACC 783
QY      788 CTTTCATTTTACCCCTGACAGGGAAGTGTCTCTCTGTTCTATACCACTGTGTTG 847
Db      784 CTTTCATTTTACCCCTGACAGGGAAGTGTCTCTCTGTTCTATACCACTATATAGTTC 843
QY      848 CCCATGTTTAAACCATTTATCTTACAGCTGAGGAATAGAGATGTCAAACTTGCCCTGAG 907
Db      844 CCCATGTTTAAACCATTTATCTTATAGCTGAGGAACAGAGATGTCAAACTTGCCCTGAG 903
QY      908 AGAAGCTTTTCCGAATAAGCTTTTCTTGA 937
Db      904 AGAAGCTTTTCCGAATAAATCTTTCTTAA 933
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Search completed: September 30, 2004, 00:31:00
Job time : 4168 secs

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Db 66 TATTGTGTGACCGTTGGCATTTGGGATGGCCATTGTGGCCGTTTATCTCTTAAGTTT 8
QY 661 TATTCTT 667
Db 7 TATTCTT 1
RESULT 2
US-09-016-434-1114
Sequence 1114, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1114:
SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1336040
US-09-016-434-1114
Query Match 27.5%; Score 265; DB 4; Length 945;
Best Local Similarity 56.0%; Pred. No. 4,3e-73;
Matches 502; Conservative 0; Mismatches 395; Indels 0; Gaps 0;

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Db 199 AACTGTCCCTCGTATATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 258
QY 254 TTGTCTCAAGAGAAACATTTATTTCTTCTCACAGGGGTATAGTCTCTCTCTCTCTCTCT 313
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QY 314 TGTCT 373
Db 319 TGTACTTTTGACAGATACAAATCTTCACTCTGCGCGCCATGCTATGATGCTATGTC 378
QY 374 GGCATCTGTACCCACTGTGTACAGATACACCATCTCTCCAGATGTTGTCTCTCT 433
Db 379 GGCATCTGTACCCCTTATTTGACAGATGATGATCTCTAGGGGATCTGTATGGGTTG 438
QY 434 TTAAGGCTGTCT 493
Db 439 ATTGTCTGTCAATCTCTGAGGCAACATGATGTTCTCTGTCACACATCTTCTCTCT 498
QY 494 TTCTGACCTTTGTGACAGACACCTGTCACTCACTGATGATGATCTCTCTCTCTCTCT 553
Db 499 ATTCTGAATATTTGACAAATATTTATTTATTTCTGATCTCTCTCTCTCTCTCTCT 558
QY 554 CTGAGCT 613
Db 559 CTGAACTATCT 618
QY 614 GTTGGATTTGGGCTGCT 673
Db 619 TTAGGGAATATTTGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 678
QY 674 ATTCTCCGCTGTAGTCTGCTGAGGAGGTCTTAAGCCTTCACTGATCTCTCTCTCTCT 733
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QY 734 ATTAATGCACTTCT 793
Db 739 CTGACTTGAAGTACATCTTCAACAGGACTCTCTCTTATTTATTTATTTATTTATTT 798
QY 794 ATTTAACCCTGACACAGGAGAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 853
Db 799 CTGATATCT 858
QY 854 TTAAACCATTAATCTTCAAGCTCTGAGAAATAGAGTGTCAACTGCTCTGAAGA 910
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RESULT 3
US-09-668-680-11
Sequence 11, Application US/09668680
Patent No. 6436703
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Wang, Jian-Rui
APPLICANT: Xue, Aidong J.
APPLICANT: Xu, Chengjun
APPLICANT: Dimaec, Radoje T.
TITLE OF INVENTION: No. 6436703el Nucleic Acids and
FILE REFERENCE: 790CIP2A
CURRENT APPLICATION NUMBER: US/09/668, 680
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: pt_fl_genes Version 2.0
 ; SEQ ID NO 11
 ; LENGTH: 1297
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (225)..(1091)
 US-09-668-11

Query Match 24.6%; Score 236.6; DB 4; Length 1297;
 Best Local Similarity 54.4%; Pred. No. 4,4e-64;
 Matches 476; Conservative 0; Mismatches 399; Indels 0; Gaps 0;

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 DB 184 ATCCAGACTGCGAGCCAGTCTTCTGGGCTGTCTCTGTCATGTGCTGTCACGGTCC 243
 QY 120 TGGGGAACCTGGGCTTGAATATCTGATAGGGCTCACTGCGCTGATATCCCATGT 179
 DB 244 TGGGGAACCTGCTCATCTCTGCGCATCAGCCCTGACTCCACCTCCACACCCCATGT 303
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 DB 364 AGATGATTTGACATGCAAACTCAGACAGAGTCACTCCATGTAAGGCTGCTGACTC 423
 QY 300 AGTTCTTCTTCTCTGTTTCTTGTCTTCTTCTGATGCTTCACTCTGCGGAGTGTG 359
 DB 424 AGATGCTTCTTCTTCTGCTTCTTCTGATGATGATGATGATGATGATGATGATG 483
 QY 360 AGGACGCTACGTTGGGATCTGTAACCACTGTTGTAACAGATCACTGCTCCCGAG 419
 DB 484 ATATCCGGTTTGGGCTATGTCACCCCTGACATCCGAAATCAATGAAACCCAGCC 543
 QY 420 TGTGTTGCTCTTCTTCTGAGGTGTCTACGGAGTGGGGGTTTGGGGCTGTGCTCAT 479
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 DB 904 TCAATTAGCTGTGTTACATCCCTCCAGAGAGATGTTGCTTCAATGATATACATG 963
 QY 840 CTGTGTGCTCCATTTTAACTTATCTACAGCTGAGAGATTAAGATGTCAAACTTG 899
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DB 1024 CCTGTGACGCTCTGACATGAGCATCATCAATCT 1058

RESULT 4
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 ; Sequence 1313, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; NUMBER OF INVENTIONS: 1490
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREMITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0002 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1313:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1438 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GENBANK
 ; CLONE: 932092
 US-09-016-434-1313

Query Match 23.8%; Score 229.2; DB 4; Length 1438;
 Best Local Similarity 54.1%; Pred. No. 1e-61;
 Matches 490; Conservative 0; Mismatches 413; Indels 3; Gaps 1;

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 DB 431 CAGATCACCTTTTGGGCTGTCTTCTGCACTATACATCTTAACTTACAGGCAATATC 490
 QY 131 GCTTATATTCCTGATAGGAGCTCACTGCTGCAATATCCCATTAATTTTCCCTC 190
 DB 491 ATCATTTGACATCATCTCCGAATTTGATTTTCTTCAACACCATATATCTTCTCTG 550
 QY 191 TTCAACTGTCTCTGATGATTTTATGTTTCTTCAAGACATATCCCAATATGCTGATG 250
 DB 551 AGCATGCTGTCTCACTTCAAGACATGATATATCATTTGCTATTTCCCAAGATGCTCTCC 610
 QY 251 AGTTTGTCTCAAGAGACATTAATTTCTTCAAGGGGTATGATGATGATGATGATGATG 310

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Db      611 AGCTCTGATGATGATGACCAAGCCAGTATGAGGAGGCTGGCCACAGATGTTCTT 670
Qy      311 TTCTGTTCTTTGTTCTTTTCTGATCTTCATCTCTGAGCGAGTGGAGACCGCTAC 370
Db      671 TTGTAACTTTGGATGACTAAGTCTCTGCTCAGACAGATGGATATGACCGCTAT 730
Qy      371 GTGGGATCTTAACCCACTGTGTGACAGATCACCAGTCTCCCCAGGTGTGTGCTC 430
Db      731 GTGGGATCTTAACCCACTGTGTGACAGATCACCAGTCTCCCCAGGTGTGTGCTC 490
Qy      431 CTTTAACTGCTGCTGACAGGATGGGGGTTTGGGGGCTGTGCTCATACAGAAATATA 490
Db      791 CTGTGCTGGGGGCTGACAGATGGGGGTTTGGGGGCTGTGCTCATACAGAAATATA 850
Qy      491 GTGTTTCACTTTTGTGACAGACACTTGTCAATCACTAAGTGTGACATCTTCCC 550
Db      851 TTCAAGTTACCTTCTGTGCTGATAAAA---GGTGGCCCACTTCTGTGACATCGGCCCT 907
Qy      551 CTTCTTGAAGCTCTGACAGGCTTTAATATATATATATATATATATATATATATAT 610
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Db      1028 ACAATCTCAAGATTTGCTTCACTGATGAGGCGGAGAAAGGCTTTTGCACCTGTGACATCC 1087
Qy      731 TACATATATGAGTTTCTTCTTTCTTTGAGGATGAGGCTTTTACGATCTTAAACCCCT 790
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Db      1148 TCAGAGAACACAGAGAACATGACAGCTGATCTGAGCTTACATCTGATCACTCCC 1207
Qy      851 ATGTTTAACTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 910
Db      1208 CTACTGAACCTGTGTATACCTGTGAATTAAGGTGTGAAGATGCTGTGTGAGG 1267
Qy      911 ACCCTT 916
Db      1268 GCTGTT 1273

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; SEQ ID NO 10
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)..(1062)
US-09-668-680-10
Query Match      23.7%; Score 228.4; DB 4; Length 1062;
Best Local Similarity 52.8%; Pred. No. 1.5e-61;
Matches 493; Conservative 0; Mismatches 441; Indels 0; Gaps 0;
Qy      2 ATGGCTGCGAGAACTCTCTCCGTCAGAGATTTATCTGACAGCTTATCCACCG 61
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Qy      122 GGGAACTGGGCTTGAATATCTGATAGGCTCAACTCTGCTGATATCCCATGAC 181
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Qy      182 TTTTCCCTCAACTGTGCTGATTTTATGTTTCTTACAGACATATCCCAA 241
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Qy      242 ATGCTGATGATTTTGTCTCAAGAAACATTTTCTTCAAGGCTGATGATGATGATGAT 301
Db      364 ATGCTGATGATTTTGTCTCAAGAAACATTTTCTTCAAGGCTGATGATGATGATGATGAT 423
Qy      302 TTTTCTCTCTGATTTTGTCTGATTTTGTCTGATTTTGTCTGATTTTGTCTGATTTTGTCT 361
Db      424 GTCTATTTCTCAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 483
Qy      362 GACCGTACGATGGGCTATGTAACCATGTTGTACAGATCAGCATCAGCATCAGCATCAGCAT 421
Db      484 GACCGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
Qy      422 TGTCTCTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
Db      544 TGTGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
Qy      482 GGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
Db      604 TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
Qy      542 ATCTTCTCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
Db      664 CTGACGTACATCTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
Qy      602 ATGTTGTGACGTTGGCATTTGGGGTGGCCATTTGTCGCTTTTATCTTATGCTTTT 661
Db      724 TTTATGACGGGTGTGTGTGGGCTTTTCCCTCTCTGAGATCATTTTCTTATTCACGA 783
Qy      662 ATCTTCTCAGCATCTCGCGTTAGTTCTGTGAGGAGCTTAAAGCTTCACTGATGAC 721
Db      784 ATGCTTATCATATAGAAAGATGCTCATCTGTGGGGAACAAAGACATTTTCCACC 843
Qy      722 TCGAGTCTCATATATGCAATTTCTTCTTCTTGTGAGAGCTTTTACGATCTC 781
Db      844 TGTGGGTCTACCTCTCTGCTGTTCTTATTTATGAGACAGGATTTGGGCTCACATTC 903
Qy      782 AAACCCCTTCCATTTTACCTCTGACAGAGGGAAGTCTCTCCCTTCTTATACACT 841
Db      904 ACTTGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
Qy      842 GTGATGCTGATTTTAACTTATATCTTACAGCTTGAAGATTAAGATGTCAACTTGGC 901
Db      964 GTCAACCCCATGTTAAACCCCTTCACTTACAGCTTGAAGAAACAGATGTGAAGGAGCC 1023

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RESULT 5
US-09-668-680-10
; Sequence 10, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong-Ji
; APPLICANT: Xu, Chongjun
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790C1P2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_fl_genes Version 2.0

```


ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (178)..(1080)
 US-09-668-680-9

Query Match 23.5%; Score 226.6; DB 4; Length 1080;
 Best Local Similarity 53.1%; Pred. No. 5.5e-61;
 Matches 481; Conservative 0; Mismatches 424; Indels 0; Gaps 0;

QY 30 CAGAGTTTACTCGAGGCTTAATCCACAGCCGGAGCTCCAGGTCCTCTTCTTC 89
 DB 107 CAGAAATCCCTCCTCGGAGCTCTCAGAGATCCAGAACTGAGCCCTCCTCCCTG 166
 QY 90 TGTTCCTAGGTTTCAACGGGTGACGGGTGAGGAGTGGGAGTGGCTTGAATCCGATAG 149
 DB 167 TGTTCCTAGGTTTCAACGGGTGACGGGTGAGGAGTGGGAGTGGCTTGAATCCGATAG 226
 QY 150 GGCCTCACTGCGCTGTCATATCCCATGATCTTTTCCCTCACTTGTCCCTGATG 209
 DB 227 GCTGACCTCCACCTCCACACCCCATGCTTCTTCTCCATCCAGCTGTGCGGCTG 286
 QY 210 ATTATAGTTTCTACAGACATCATCTCCCAAAATGCTAGTGTTCCTCAAGAGAGA 269
 DB 287 ACATGCTTCACTGCGGAGTGGTCCCAAGATGATGAGATGAGATGAGATGAGCA 346
 QY 270 ACATATTTCTTCAACAGGTTGATGATGATGATGATGATGATGATGATGATGATG 329
 DB 347 GAGTATCTCTTATGCGGCTGCGCTGAGACAGATGCTTCTTCTTCTTCTTCTTCT 406
 QY 330 CTGATCTCTTCACTGCTGCGGAGTGTGAGAGACCGTACGTTGGGATCTGTACCCAC 389
 DB 407 TAGAAGACATGCTCTGACAGTATGAGGCTTATGACCGATGTTGCGCATGCTACCCC 466
 QY 390 TGTTCCTAGGTTTCAACGGGTGACGGGTGAGGAGTGGGAGTGGCTTGAATCCGATAG 449
 DB 467 TGTTCCTAGGTTTCAACGGGTGACGGGTGAGGAGTGGGAGTGGCTTGAATCCGATAG 526
 QY 450 GGATGCGGTTTGGGGCTGCTGCTATACAGAAATATATATATATATATATATATAT 509
 DB 527 TGTTCCTAGGTTTCAACGGGTGACGGGTGAGGAGTGGGAGTGGCTTGAATCCGATAG 586
 QY 510 CAGACAACTGCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 569
 DB 587 AGAATGAGAAATCTCAATTTTGTGAGACCATCTCAATCTTCAATCTTCAATCTTCA 646
 QY 570 ACGGCTCTTCAATTAATGCTGCTGATCTTATGTTGATGATGATGATGATGATGAT 629
 DB 647 CTGACAGTATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 706
 QY 630 CCAATGTTCCGTTTATCTCTTATGATTTTATCTTCCAGATTTCCGCTTATGTT 689
 DB 707 CCAATGTTCCGTTTATCTCTTATGATTTTATCTTCCAGATTTCCGCTTATGTT 766
 QY 690 CTGCTGAGGAGGCTCAATGCTTCACTGATGCTGATGCTGATGCTGATGCTGATGCT 749
 DB 767 CATAGATAGGAATGCTCAATGCTTCTCACTGATGCTGATGCTGATGCTGATGCTGAT 826
 QY 750 TTTTCTTTGGGTCAAGAGCTTTTACGTAAGTCAATCCCTCTTCAATTTTACCTTGACC 809
 DB 827 TATTTTATGGAACGAGGCTATGCGGTGATGCTGATGCTGATGCTGATGCTGATGCT 886
 QY 810 AGGGAAGAGTGTCCCTCTCTTATTAACGATGCTGATGCTGATGCTGATGCTGATGCT 869
 DB 887 ATGCTGAGTGTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 946
 QY 870 ACAGCTGAGGAATGAGATGCTCAATCTTCCCTGAAAGAACTTTTCCAGATATAGCT 929
 DB 947 ACAGCTGAGGAATGAGGAATGCTCAATGATGCTGATGCTGATGCTGATGCTGATGCT 1006
 QY 930 TTTCT 934
 DB 1007 AATCT 1011

RESULT 8
 US-08-748-506-8
 Sequence 8, Application US/08748506
 Patent No. 6159707
 GENERAL INFORMATION:
 APPLICANT: Rometic et al.
 TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 74940
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5700
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 966 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-748-506-8

Query Match 22.7%; Score 218.4; DB 3; Length 966;
 Best Local Similarity 52.1%; Pred. No. 1.9e-58;
 Matches 486; Conservative 0; Mismatches 446; Indels 0; Gaps 0;

QY 11 GAGACTCTCTCTCCGTGACAGATTATCTCGAGGCTTAATCCACAGCCGGAGCTC 70
 DB 28 GAGAAATGTTGTCTGTCAAAAGTTTGCATTTGCAAGTTCTGTAGGTCCTGGAGAA 87
 QY 71 CAGTCCCGTCTTCTCTGTTTCTAGTTTCTACGCGGTACGAGTGGGAGAACTG 130
 DB 88 TGTCTCTCTGTTTACCTTATCTTCTATGTTCTTATGATCACTAAGAAATGCT 147
 QY 131 GCTTGATATCTTATAGGCTCACTGCTGCTGATATCCCATGTTTCTTCCC 190
 DB 148 CTCATAGCCCTGTATTTTATGATGATGATGATGATGATGATGATGATGATGATG 207
 QY 191 TTCATCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
 DB 208 GCCACTGCTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 267
 QY 251 AGTTTGTCTCAAGAGAAATATTTCTTCAAGGTTGATGATGATGATGATGATGATGAT 310
 DB 268 AGCTTGTGAGTGAAGCCCGAGAGATCTTTCAGGTGGGATGTCACACAGATGTTTTC 327
 QY 311 TTTCTTTCTTGTCTTTTCTGAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 370
 DB 328 TTTATTTCTTTGATTAAGTGAAGTCTTATTTGAGGCTGCTTGTGACGCTAT 387
 QY 371 GTGGCACTGTAAACCACTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 430


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Db      388 ATGGGATATATGTTCCCACTCCATATGCAACCCGAATGAGCTGAGGATATGAGCCAC 447
Qy      431 CTTTAACTGGGTGTCTAGCGGATGGGGGTTTGGGGCTGGGCTCAACAGAAATATA 490
Db      448 TTGGCAATGTTTCAATGGGTATGAGATGATAGAGTGGGAGACCAATTTTATT 507
Qy      491 GTGTTTCTACCTTTTGTGTCAGAACACTTGTCACTACTACATGATGTGACATCTTCCC 550
Db      508 TTCTCTTAATCTTCTGTGAGCCCTGTGAGATAGACACTTCTTGTGATCTTCACT 567
Qy      551 CTTCTTGAAGCTCTCTGTGCAAGGCTTTAATGATTAATGCTGTGATCTTTATTTGTG 610
Db      568 CTCCTGGCACTTGGCTGTGTGATATCCCAATGAGGCTGCATCTTGTGTAGTT 627
Qy      611 ACCGTTGGCATGGGGGTGCCCATGTTGGCTTTTATCTTTATGTTTATCTTCC 670
Db      628 GTCTCTGCAATCTAGCCCTTTTGTGATCATTATCTTATGTCAAGATTTCTGTT 687
Qy      671 AGCATTTCCGGGTAGTTGTGCTGAGGAGGCTTAAAGCTTGAAGTGCAGCTCC 730
Db      688 GCAGTCTGATATGCTTCACTGAGGGGCGCACAAAGCCCTTCAACCTGTCTCC 747
Qy      731 TACATTAATGCACTTCTTCTTTCTTGGGTCAAGAGCTTTAGAGCTCAACCCCT 790
Db      748 CACCTAATGTATGACACTCTTTTATAGGCTGAGATCTGTATCTTATTTGAGCTTAG 807
Qy      791 TCCATTTTACCCCTGAGCAGGGAAGTCTCTCCCTGTCTTATACACTGTGTGCCC 850
Db      808 TCTAGCAGCTACACAGAAATGACAAACTTGGCCCTCTTCTACACAGAGTACATCC 867
Qy      851 ATGTTTAACTTAATCTTACAGCTGAGGATTAAGATGTCAACTTCCCTGAAGAA 910
Db      868 ATGTTAACTTATCTTATAGATTTAAGAACAGATGTCAAGGACAGCTGAGAA 927
Qy      911 ACCTTTCCAGAAATAGCTTTCTGAAAAA 942
Db      928 ATTCTGACCTGAAAAAATTCTGTCAATTA 959

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RESULT 9
 US-09-016-434-1413
 ; Sequence 1413, Application US/09016434
 ; Patent No. 6500938
 ; GENERAL INFORMATION:
 ; APPLICANT: Janice Au-Young
 ; APPLICANT: Jeffrey J. Sellhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1490
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016,434
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071

```

; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1413:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9516319
; US-09-016-434-1413

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Query Match 22.7%; Score 218.2; DB 4; Length 1282;
 Best Local Similarity 52.9%; Pred. No. 2,7e-58;
 Matches 469; Conservative 0; Mismatches 418; Indels 0; Gaps 0;

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Qy      25 CGTACAGAGTTATCTCGAGGCTTAATCCACAGCCGAGACTCCAGGTCCTCCGCTT 84
Db      191 CATGCTGAGTCAATCTCTGAGGCTTCTGAGGAGCGCAGGGCTGACGCAATGCTT 250
Qy      85 CTTCTGTTCTAGGTTCTACGGGCTACGGGTGAGGGAACCTGAGCTTGATATCT 144
Db      251 TGTGCTCTCTCTTGTGCTAAGCTGTCACGGTCAGGGGCAACTCAGATCTCGAGC 310
Qy      145 GATAGGCTCAACTCTGCGCTGATATCCCATGTAATCTTTTCCCTCAACTGTCCCT 204
Db      311 TGTCTGTGAGGCCAAATCCACACCCCATGTAATCTTCTTGGGGAACCTATAGT 370
Qy      205 CGTATGTTTATGTTCTCTACAGCATCATCCCAATGCTAGATGATTTGTCTAG 264
Db      371 GCTGATGTTGGGTGATCAGGCTCACTGTCATCATGATGATGATGCTCTGCTCCG 430
Qy      265 GAAGAACTTATTTCTTCAAGGCTGTATGATGATGCTTCTTCTTCTTCTTGT 324
Db      431 CAAGGCTCAGTCTCTGTGGGCTCTTACCCAGCTCTTCTTCTTCACTGTGCT 490
Qy      325 CTTTCTGAGCTTCACTCTGCTGAGGAGTGGAGAGCGCTACGAGGAGCTGTAA 384
Db      491 TGAAGTGAAGCTTCTCTGCTGACCGCATGCTATGACCAATCTCTGCGCATCTGCG 550
Qy      385 CCACTGTTGTACAGATACCATGCTCTCCCAAGTGTGTTCTCTTCTTCTGAGGT 444
Db      551 GCCCTCACTTACAGCAACCCGATGAGTCAAGATGTTGAGTGTGCTGCTC 610
Qy      445 CTACGGATGGGGGTTTGGGGCTGTGGCTCATAGGAAATPAGTGTCTCACCT 504
Db      611 CTGGCTGTGCTTTCACCAAGCACTGACCCACAGCTGTGCCATGTCCAGCTCACTT 670
Qy      505 TTGTCAGAACACTTGTCAATCACTACATGATGTGACATCTTCCCTTCTGAGCTCTC 564
Db      671 CTGTGCCCCAATGATGATCACTTCTACGTGACCTCCCAAGCTCTTCCAGCTCTC 730
Qy      565 CTGACAGGCTCTTACATTAATGCTGTGATCTTTATTTGTGTGACCGTTGGCATGG 624
Db      731 CTGTCTCAGCAACCCCACTCAATGAGCTCTCTTGTGCTGTGAGTTTATATAGGAG 790
Qy      625 GGTGCCAATGTTGGCGTTTATCTTATGTTTATCTTTTCCAGATTTCTCCGCT 684
Db      791 TACCCCAATGCTCTCATTTGATCTCTTATACAGCTGAGAGTGAAGTCTCGCAAT 850
Qy      685 TAGTCTGCTGAGGAGGCTTAAAGCTTGAAGTGTGAGCTCTTCAATATTTGAGT 744
Db      851 TCGCTGTGAGAGGAGAGAGAAAGCTTCCCAATGATGCTCTCCCACTCACTGTGT 910
Qy      745 TTCTCTTTTCTTGGGTGAGAGCTTTTACAGTCAAAAGCTTCAATTTACCTTCCCT 804
Db      911 TGCATATCTATGATGATGATCTTATCTTATGATGATGATGATGATGATGATGAT 970
Qy      805 GCACGAGGGAAGTGTCTCTCTCTTCTTATACAGCTGTGTGCTGATTTTACCATTT 864

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Db 971 AGACAGAGATTAAGCTGTGGAAATTTTCACACTGTATCATATCCATGCTGACACCCAT 1030
Qy 865 AATCTACAGCTTGAGAAATTAAGATGTAACCTTGCCCTGAAGAGA 911
Db 1031 CATCTACAGCTTGAGAAACCTTGATGTGACAGATGCTCATCTGAGAGA 1077

RESULT 10
US-08-827-291A-1
; Sequence 1, Application US/08827291A
; Patent No. 5874243
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Sathie, Ganesh
; TITLE OF INVENTION: NOVEL OLRCIS RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: PA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,291A
; FILING DATE: 28-Mar-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GPS0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5015
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-827-291A-1

Query Match 21.9%; Score 210.6; DB 2; Length 1290;
Best Local Similarity 51.9%; Pred. No. 6.6e-56;
Matches 474; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

Qy 2 ATGCGTGGCCGAGAACTCTCTCCGTGACAGAGTTTCTCGAGGCTTAATCCACAG 61
Db 296 ATGCGAGGAGAAATTCACCTTCACTCCGACTTCACTTCCGGAATCTTCAATCAC 355
Qy 62 CCGGAGCTCCAGTCCCGCTTCTCTCTCTAGATTTCACGGGAGTCAAGGGTGTG 121
Db 356 AGCCCAACCCACACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 415
Qy 122 GGAAGACTGGGCTTGATTAATCTGTAAGGGCTCACTCTGCGCTCATATCCCATGTAC 181
Db 416 GGAAGACTGTGATGATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 475
Qy 182 TTTTCCCTTCACTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 241
Db 476 CTCTCTCTCTCACT 535
Qy 242 ATGCTGATGATTTTGTCTCAAGAGAACATATTTCTTCAAGGGGTATGACTGAC 301

Db 536 ATGGCCCTTCAACTACCTGTCTGACAGAGTTCATTTCTATAGCTGTGTGCCACAA 595
Qy 302 TTTCT 361
Db 596 ATTTCTTCTATACATCTACTGCTTGGCTTGAATGCTTCTTGTGCTGTATGCTTAT 655
Qy 362 GACGCTACGTGGGCACTGTATACCCACCTGTGTATACAGATCAACATGTCCTCCAGGTG 421
Db 656 GACGCTACACTGCACTTGTCCACCTGTATACAGATCAACATGTCATGAGCCCTAAAT 715
Qy 422 TGTTCCTCTTCTTACTGGGTCTCTACGGATGGGGGTTTTGGGCTGTGCTCTATA 481
Db 716 TGTGACTTATGACCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 775
Qy 482 GGAATATATAGTCTTCTCACTTTTGTGACAACTTGTCAATCACTACATAGTGTGAC 541
Db 776 GTAGCCACATTTCT 835
Qy 542 ATCTTCTCTCTTCTTGAAGCTCTCTGCAACGGCTCTTAATTAATGTCCTGTATCTTT 601
Db 836 TTAACCTTCTCTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 895
Qy 602 ATGTGTGACCGTGGCAATGGGGTGGCCATTTGTCCTTTTATCTTATAGTGT 661
Db 896 ATTTGCTATATATATGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 955
Qy 662 ATCTTCTCAAGATTTCTCCGCTGTAATGTCGTGAGGGAGGCTTAAGCCCTTCAGTAC 721
Db 956 GTATATCTGCTGTCTATCAATCAATGAGATCTGAGAGGGGCTCTGCAAGCTTTCAGAC 1015
Qy 722 TGCAGCTCTCAATATATGACATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 781
Db 1016 TGTTCCTCTCACTCTATGCTGTGGAATGTTCTATGAGCAGGTTTGTCTATGATATA 1075
Qy 782 AAACCCCTTCCATTTTACCCCTGACACAGGGAAGTCTCTCTCTCTCTCTCTCTCT 841
Db 1076 CAGCCACATCTGATGCTCTCCCAAGAGAGCAAGCTGTGTCTATCTACACATC 1135
Qy 842 GTGTGCTCCATTTTAACCATTAATCTTAACGCTGAGGAATTAAGATGTCAACTTGGC 901
Db 1136 CTCACTCCCATCTGAATCCCTCTCACTTAACACCTCCGCAACAGGAATGACAGAGA 1195
Qy 902 CTGAAGAGAACT 914
Db 1196 TTCAATGAATCT 1208

RESULT 11
US-09-546-986A-1
; Sequence 1, Application US/09546986A
; Patent No. 6635741
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. 6635741e1 G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42)..(974)
; OTHER INFORMATION: human breast cancer amplified G-protein coupled

OTHER INFORMATION: receptor 1 (BCA-GPCR-1)
US-09-546-986A-1

Query Match 21.8%; Score 210.2; DB 4; Length 1035;
Best Local Similarity 52.0%; Pred. No. 7.7e-56;
Matches 470; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

22 CTCGAGACAGATTATCTTCGACAGGCTTAATCCACAGCCGGGACTCCAGTCCCGT 81
53 CTCCTTAAGCCTTCATCTTCGGGTGTCTGACAGGCGGTGGTAACTCCCTCT 112
82 CTCTTCCTCTTCAAGTTTCTAAGCGGTACAGGTGGGGAACCTGGCTGATAT 141
113 CTCTTGAGTCTCTCGCTGCTGCTATGTGTGGCCAGTGGGGAAGTGCCATCATCT 172
142 CCGATAGAGGCTCAACTCTGCGCTGATATCCCAATGACTTTTCCCTTCAGTGTGC 201
173 GCGATCCGCGGTGATATCCCTCACTCCAGCCCAATGATCATCTTCTGAGTCACTGTGC 232
202 CCGTAGATTTTAAATTCTCTTCAAGACATATCCCAAAATGCTGATGAGTTTGTCTC 261
233 CTCTCGAGACTCTGTACACACACAGAGTCCCTCAGATGCTGTGCTACATGGGAG 292
262 AAGGAAGACATTAATTCCTTCAAGAGGTATAGTCACTTCTTCTCTGTTTCTT 321
293 TTCCCAAGAAACCATAGCTATAGAGGCTGCACTGTGCATATGACAGTCTTCCACTGCT 352
322 TGTCTTTTCTGAGTCTTCACTCTGTGCGATGAGTGGAGAACCGCTACGTGGGATCTG 381
353 GGGATGACAGAGTGCATGCTCTGCGCCGCAATGCGCTGGAACCGGTACGTGGCAGCTG 412
382 TAACCACTGTGTATACATACATCACTGTCTCCCAAGGTGTGTCTCTTTACTGGG 441
413 CAAGCCCTGCACTATGCGGTCTCAAGACGCTGCTCTGTGCAAGAGTGTGCTCT 472
442 TGTCTACGGGATGGGGTTTTTGGGGCTGTGCTCAATAGAGAAATATAGTCTCTCA 501
473 GGGCTGCTCAAGGTCTGCGGAACCTCTGCGAGGTGTGCTGACGATGCAATGTGC 532
502 CTCTTTGTGACACACCTTGTCAATCACTAATGTGTGATCTTCCCTCTTGTAGCT 561
533 ATCTGCGGGCGGAGGTGCTGAACAATTTTCTGTAGGTGCCGCGGTATCAAGCT 592
562 CTCTGCAAGGCTCTTACATTAATGCTGTGATCTTATATGTGTGACCGTGGCAT 621
593 GTGTGTGCTGACACCGCTATGATACACATACAGTGGTGTGTGTGTGTGTGTGTGT 652
622 TGGGGTGGCCATTTGTGCGGTTTTTATCTGTATGTGTGTATTTCTTTCCAGCATTTCCG 681
653 GTGTGTGCGGCTGCTCATCTTCTCTCTATGCTTATGTGTGTGTGTGTGTGTGTGT 712
682 CGTTATGTTCTGAGGAGGAGGTCTAAGGCTCAGAGTGCAGGCTCTCAATATATG 741
713 GATCACTGCTTCAAGGAGACACAAAGGCTTTGGAGCGTGTCTTCCACTGATGAT 772
742 AGTTTCTCTTTCTTTGGTCAAGAGCTTTTACGTAACCTCAAAACCCCTTCATTTTACC 801
773 CGTCTCTCTTCTTACTACTGAGATTACATGATATCTGAGCCCTTCCAGCTACTC 832
802 CCGAGACAGGGGAAAGTGTCTCTCTGTCTTATACAGTGTGTGTGTGTGTGTGTGTGT 861
833 CCAAGACAGGGGCAATTTATTTCTCTCTTATTCATATATCAACCCCACTCTCAATCC 892
862 ATTATATCAAGCTGAGATTAAGATGATCAAACTTGCCTGAAGAACTTTTCCAG 921
893 CTCTACTACACCTGAGAAATTAAGATATAGAGGGGCTCTAGAGGATCTTGTGGCAG 952
922 AAT 924
953 GAT 955

RESULT 12

US-09-524-730-1
Sequence 1, Application US/09524730
Patent No. 663873
GENERAL INFORMATION:
APPLICANT: Powers, Scott
APPLICANT: Yang, Jianxin
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: No. 663873e1 G-Protein Coupled Receptors
FILE REFERENCE: 018781-004710US
CURRENT APPLICATION NUMBER: US/09/524,730
CURRENT FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1035
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (42)..(974)
OTHER INFORMATION: human breast cancer amplified G-protein coupled
OTHER INFORMATION: receptor 1 (BCA-GPCR-1)
US-09-524-730-1

Query Match 21.8%; Score 210.2; DB 4; Length 1035;
Best Local Similarity 52.0%; Pred. No. 7.7e-56;
Matches 470; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

22 CTCGAGACAGATTATCTTCGACAGGCTTAATCCACAGCCGGGATCTCCAGTCCCGT 81
53 CTCCTTAAGCCTTCATCTTCGGGTGTCTGACAGGCGGTGGTAACTCCCTCT 112
82 CTCTTCCTCTTCAAGTTTCTAAGCGGTACAGGTGGGGAACCTGGCTGATAT 141
113 CTCTTGAGTCTCTCGCTGCTGCTATGTGTGGCCAGTGGGGAAGTGCCATCATCT 172
142 CCGATAGAGGCTCAACTCTGCGCTGATATCCCAATGACTTTTCCCTTCAGTGTGC 201
173 GCGATCCGCGGTGATATCCCTCACTCCAGCCCAATGATCATCTTCTGAGTCACTGTGC 232
202 CCGTAGATTTTAAATTCTCTTCAAGACATATCCCAAAATGCTGATGAGTTTGTCTC 261
233 CTCTCGAGACTCTGTACACACACAGAGTCCCTCAGATGCTGTGCTCAAGTGTGC 292
262 AAGGAAGACATTAATTCCTTCAAGAGGTATAGTCACTTCTTCTCTGTTTCTT 321
293 TTCCCAAGAAACCATAGCTATAGAGGCTGCACTGTGCAATATGCAATCTTCCACTGCT 352
322 TGTCTTTTCTGAGTCTTCACTCTGTGCGATGAGTGGAGAACCGCTACGTGGGATCTG 381
353 GGGATGACAGAGTGCATGCTGTGCGCCGCGCATGCGCTGAGCGCTACGTGGCAGCTG 412
382 TAACCACTGTGTATACATACATCACTGTCTCCCAAGGTGTGTGTGTGTGTGTGTGT 441
413 CAAGCCCTGCACTATGCGGTCTTCAATGAGGCTGTGCTGTGAGAGTGTGTGTGTGT 472
442 TGTCTACGGGATGGGGTTTTTGGGGCTGTGCTCATACAGAAATATAGTGTCTTAC 501
473 GGGCTGCTCAAGTGTCTTGGCAACTCTTGTGTGAGGTGTGCTGAGAGTGTGCAATGCC 532
502 CTCTTTGTGACACACCTTGTCAATCACTAATAGTGACATCTTCCCTTCTGAGCT 561
533 ATCTGCGGGCGGAGGTGCTGACACATTTTCTGTAGGTGCGGCGGTGATACACT 592
562 CTCTGCAACGCTCTTCAATTAATGTCTGTGATCTTTATGTGTGACCGTGTGAT 621
593 GTGTGTGCTGACACCGCTATGATGACACATATGAGTGTGTGTGTGTGTGTGTGTGT 652
622 TGGGGTGGCCATTTGTGCGGTTTTTATGCTTATAGGTTTATCTTCCAGATTTCCG 681
653 GTGTGTGCGGCTGCTCATCTTCTCTCTATGCTTATGTGTGTGTGTGTGTGTGTGT 712

QY 682 CGTTAGTTCTGTCAGGAGGCTGTAAGCCTTCACTAGTCTGAGTCTCTACATATTGC 741
DB 713 GATCCAGCTCTCCAAAGGAGGACACAAAGGCTTTGAGAGCTGTCTCTCCACCTGAT 772
QY 742 AGTTCTCTTTTCTTTGGTCCAGGAGCTTTTACGTCTCTCAACCCCTTCCATTTTAC 801
DB 773 CGTCTCTCTCTTTTACCTTACCTTCCGATTTACATGATCTGACGCCCTTCCAGCTACTC 832
QY 802 CCTGACCAAGGAGAAAGTGTCTCTCTCTCTTCTATACACTGTGTGCTCCATTTTAAACC 861
DB 833 CCAAGAGCAGGAGCAATTTATTTCTCTCTTCTATTCATATACCCCCACCTCTCATTC 892
QY 862 ATTAATCTACGCTTGAAGATTAAGATCTCAACTTGTGCTCCGAGAGAACCTTTTCCAG 921
DB 893 CTTCACCTACACCTGAGAAATTAAGATTAAGAGGAGGCTCTGAGAGAGCTTGTGCGAG 952
QY 922 AAT 924
DB 953 GAT 955

RESULT 13
US-08-748-506-5
; Sequence 5, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,506
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,751
; FILING DATE: 09-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 74940
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5600
; TELEFAX: 312-616-5700
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 966 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-748-506-5

Query Match 21.6%; Score 208.4; DB 3; Length 966;
Best Local Similarity 51.4%; Pred. No. 2.7e-55;
Matches 479; Conservative 0; Mismatches 453; Indels 0; Gaps 0;

QY 11 GAGAACTCTCTCTCGTGAAGAGATTAATCTCTGAGAGCTTATCCACGAGCCGGAGCTC 70
DB 28 GAGAACTGTTGATCTGCAACACTTTGCAATTTGCAAGTTCTCTGAGAGTCTCTGAGAA 87
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QY 131 GGTGTGTAATTCCTGATAGGAGCTCAACTCTGCGCTGATATCCCAATGATCTTTTCCCC 190
DB 148 CTATAGTCT 207
QY 191 TTCAACTGTCT 250
DB 208 GCAACTGTCT 267
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QY 311 TTCTGTTCT 370
DB 328 TTGCAATTTTCT 387
QY 371 GTGGGATCTGTAACCCACTGTTGTATACAGATCACATGATCTCTCCAGGAGTGTGTCTC 430
DB 388 ATGGCCATAGTCT 447
QY 431 CTCTTCTGAGGAGTCTAGGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 490
DB 448 TTGGCAATTTCT 507
QY 491 GTGTTTCTCACTTTTGTGCAACAACCTTGTCAATCACTATGATGTGTACATCTTCC 550
DB 508 TTCTCTCTCAACTCTCTGTGAGCCCTGTGAATATAGACCACTTCTGTGTACCTTCCACT 567
QY 551 CTCTTGTGAGCT 610
DB 568 CTCTGTGACCTGCTCTGTGAGATATATCCAAAGAGGAGGAGGAGGAGGAGGAGGAGG 627
QY 611 ACCGTGAGATTGGGAGTGGCCATTTGTGCGCTTTTATCTTATCTTATGTTTATCTTCC 670
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QY 671 AGCATTTCTCGGCTTATGTTCTGTGAGGAGGAGCTTAAAGCCTTGTAGTGTGAGCTCC 730
DB 688 GGAGTGTCTCTGTATGCTTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 747
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DB 748 CACCTACTGTATGATCACTTTTATGAGCTGATGATGATGATGATGATGATGATGATG 807
QY 791 TCCATTTTACCCCTGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 850
DB 808 TCTAGCACTCAACGAGATGAGCAAAATTTCTGAGGCTCTCTCTACAGATGATGATGAT 867
QY 851 AGTTTAAACCAATTAATCTGACGCTGAGGAGATTAAGATGCAAACTTGCCTGAGAGA 910
DB 868 ATGCTGAACTTATCATATGATTTTAAGAGCAAGAGAGATCAAGGAGCAGCACTGAGAGA 927
QY 911 ACCTTTTCAGATTAAGCTTTTCTTGAAGAAA 942
DB 928 ACTGTGGGCTGAAGAAAATTTGTCAATTA 959

RESULT 14
US-08-748-506-6
; Sequence 6, Application US/08748506
; Patent No. 6159707
; GENERAL INFORMATION:
; APPLICANT: Ronnelt et al.
; TITLE OF INVENTION: NOVEL SPERM RECEPTORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voigt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US

ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-6

Query Match 21.5%; Score 207.4; DB 3; Length 966;
Best Local Similarity 51.3%; Pred. No. 5,6e-55;
Matches 478; Conservative 0; Mismatches 454; Indels 0; Gaps 0;

QY 11 GAGACTCTCTCCGTCAGAGATTATCTCCGACGGCTTATCCACGCCGGGATCTC 70
DB 28 GAGATAGTTTGTCTCAAGCGTTTGCATTGCGCACTTCTGAGGTCCTTGAGAA 87
QY 71 CAGGTCGGCTCTTCTCCGTTTCTAGGTTCTACGCGGTGACGGTGGGGAACCTG 130
DB 88 TGGTCTCTCTGTCACCTCATCTTCTCATAGTTTCTAGTATCACTAAGGAAATGCT 147
QY 131 GGGTATATCTGTATAGGCTCACTGCGCTGATATCCCATGTTCTTTTCCC 190
DB 148 CTGATAGCCCTTCTGATGATGACATCTCTACACACCCCATGTTCTTTCTG 207
QY 191 TTAACTTGTCTCTGATATTATTTCTCTACACACATATCCCAATGCTGATG 250
DB 208 GCCAACTGTCTCTCTGAGATTGCTATCTGCTGATACCCCAAGATGCTGAG 267
QY 251 AGTTTGTCTCAGAGAAACATTATTTCTTCCACAGGGTGTATGATGAGTTCTTCT 310
DB 268 AGCTTGTGTAGGCGGAGAGATCTTAGGGAGGAGATGCGCACAGATGTTTTC 327
QY 311 TTCTGTTTCTTCTCTTTTCTGAGTCTTCTCATCTGTGCGGATGTTGAGAGACGCTAC 370
DB 328 TTCACTTTTGTGCAATGATGATGCTGCTATTTGCGACCGCATGCGCTTTGACGCTGC 387
QY 371 GTGGGATCTGTAAACCACTGTTGTACAGATCAACCATGCTCCAGGTGTTTGTCTC 430
DB 388 ATGGGCAATATGCTCCCACTCCACTATGCAACCCGATAGTGTAGGATATGTCCT 447
QY 431 CTTTACTGGGTCTACAGGATGGGGGTTTGTGGGCTGTGCTCATACAGAAATATA 490
DB 448 TTGGCAATTTTTCATGGGAAATGGGATGATGATGATGATGATGATGATGATGAT 507
QY 491 GTGTTTCTACCTTTTGTGAGACCACTTGTCAATCACTACATGATGATGATGATGAT 550
DB 508 TNCCTTGAACCTTGTGAGACCTTGTGAGATAGACCACTTCTTCTGTGACCTTCCACT 567
QY 551 CTTTCTAGGCTCTCTGCAACGCTCTTACATAAATGCTGTGCTATCTTTATTTGTTG 610
DB 568 CTCCTGCACTGTGCTGTGATATACATCCCAAGAGGCTGCCATCTTTGTGGCAGCA 627
QY 611 ACCGTGGCATGGGGGCCCATTTGTCGCTTTTATCTCTATAGTTTATCTTTTCC 670

DB 628 ATCTCTGATATATAGTCCATTTTGTGATCTTATTTATATGATGAAATTCCTGTT 687
QY 671 AGCATTCCTCGGCTTATGTTCTGTGAGGCGAGTCAAGCCTTCACTGATGAGCTCC 730
DB 688 GCAGTCTGTGATGCTTCTTCACTGAGGGCGGCATTAAGCTTCTTCCACTGTCTCA 747
QY 731 TACATATGACATTTCTTCTTTCTTTGAGTCAAGAGCTTTTACGTAACCTCAACCCCT 790
DB 748 CACCTACTGTATGACACCTTTTATGCTGTGTCTTCACTTATTTGAGGCCAAG 807
QY 791 TCCATTTTACCCTGAGCAGGGAAGTCTCCCTGTTCTATACCACTGTGTGCTCC 850
DB 808 TCTAGCCACTACAGAAATGACAACTTGGCCCTCTTCAACAGAGATGACATCC 867
QY 851 ATGTTTAACTTATATCTACAGCTGAGGAATAGATGTCAACTTGCCTGGAAGCA 910
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QY 911 ACCTTTCCAGATTAAGCTTTCTTGAAAAA 942
DB 928 ACTCTGACCTGAAAAAATTAATGTAATTA 959

RESULT 15
US-09-016-434-1056
Sequence 1056, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhammer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1056:
SEQUENCE CHARACTERISTICS:
LENGTH: 1990 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91041044
US-09-016-434-1056

Query Match 21.5%; Score 206.8; DB 4; Length 1990;

Best Local Similarity 51.8%; Pred. No. 1.4e-54;
Matches 469; Conservative 0; Mismatches 437; Indels 0; Gaps 0;

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Db      496 GGCCATGATATCAAAAGCTCCACACCGGGCTTCCCTTCGCGCTTCTGAAACACC 555
QY      64 GGGACTCCAGGTCCTCCCTTCTTCTGTTTCTAGTTTCTAGCGGCTCAGGTTGG 123
Db      556 AAGGCTGGAGAGCTCTTCTGATGATCATCTTCTACCTACCTACCTAGTGG 615
QY      124 GAACCTGGGCTTGATATCTGATAGGCTCACTCGCTGATATCCCATGACTT 183
Db      616 CAACACATCATCATCTGCTGCTGCGCTGACACAGCTCCACTCTCCATGACTT 675
QY      184 TTTCCTTCAACTGCTGCTGCTGATTTAGTTTCTTCAAGACATCATCCCAAT 243
Db      676 TTTCCTTCAACTGCTGCTGCTGATTTAGTTTCTTCAAGATTTGTTCCCAAT 735
QY      244 GCTGATGATTTGCTCAAGAGACATTTATTCCTTCAAGGCTGATGATGACTT 303
Db      736 GCTGACCAACTCTGGGCCCCAAGACATCATCTGCTGCTGCTGCTGCTGCTGAT 795
QY      304 CTTCTTCTTCTGTTCTTCTTCTTCTTCTGATCTTCACTCTGCGGATGAGAGA 363
Db      796 CTTCACTTCTCTGCTGCTGCGGACACTGAGCATCTCTCATGAAGATGCTTTGA 855
QY      364 CGGCTAGCGGACATCTGATACCACTGTTGATACCATCATGCTCTCCAGTGTG 423
Db      856 TCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 915
QY      424 TTTCCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
Db      916 CTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
QY      484 AATATATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
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QY      664 TCTTCCAGCATCTCCGCGTTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
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QY      844 GGTGCCCATGTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 903
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QY      904 GAAGAG 909
Db      1396 CAGGAG 1401
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Search completed: September 30, 2004, 01:24:09
Job time : 95 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2004, 22:53:21; Search time 3085 Seconds
(without alignments) 9321.647 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 ataggctgcgagaaactcctt.....ttttagaacaagaaagaga 963

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: em_gss_hum:*
18: em_gss_inu:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_pig:*
27: em_gss_vil:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	691.6	71.8	933	AY407109	Homo sapi
2	623	64.7	903	AY405609	Homo sapi
3	602.8	62.6	933	AY407111	Mus muscu
4	580.6	60.3	799	AY407110	Pan trogl

RESULT 1	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AY407109	Homo sapiens ORB12 gene, 933 bp, DNA linear	AY407109	GI:39763080	Genomic survey sequence.	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.	Interfering nonneutral evolution from human-chimp-mouse orthologous gene clones	
AY405610	Pan trogl	AY405610							
AY405611	Mus muscu	AY405611							
AY405657	Homo sapi	AY405657							
AY405659	Mus muscu	AY405659							
AY419056	Pan trogl	AY419056							
AY419055	Homo sapi	AY419055							
AY419057	Mus muscu	AY419057							
CE158635	tigr-gss-	CE158635							
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AZ255774	RPCT-23-1	AZ255774							
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CB174480	OR_20E1H1	CB174480							
AQ0503914	RPCT-11-2	AQ0503914							
CA880338	KO982C03-	CA880338							
CE184619	tigr-gss-	CE184619							
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BZ201201	CH230-303	BZ201201							
CB173618	OR_2021B1	CB173618							
AY405614	Mus muscu	AY405614							
CA881328	KO989P04-	CA881328							
AY405612	Homo sapi	AY405612							
AZ016145	RPCT-23-3	AZ016145							
BZ207385	CH230-487	BZ207385							
BZ125252	CH230-238	BZ125252							
AY402814	Pan trogl	AY402814							
AY402814	Homo sapi	AY402814							
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AY402815	Mus muscu	AY402815							
CB174356	OR_2041F0	CB174356							
AY404165	Mus muscu	AY404165							
AY415715	Mus muscu	AY415715							
BH342817	CH230-64F	BH342817							
AY405000	Homo sapi	AY405000							
AY405001	Pan trogl	AY405001							
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AY405605	Mus muscu	AY405605							
BB201968	BB201968	BB201968							
CB174038	OR_2032D0	CB174038							
AY401567	Mus muscu	AY401567							
CB173917	OR_2019A0	CB173917							

ALIGNMENTS

RESULT 1
AY407109
DEFINITION
Homo sapiens ORB12 gene, 933 bp, DNA linear
ACCESSION
AY407109
VERSION
GI:39763080
KEYWORDS
Genomic survey sequence.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE
Interfering nonneutral evolution from human-chimp-mouse orthologous gene clones
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 933)
AUTHORS
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES Location/Qualifiers

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/locus_tag="HCW2781"

ORIGIN

Query Match 71.8%; Score 691.6; DB 29; Length 933;
Best Local Similarity 84.0%; Pred. No. 2e-154;
Matches 781; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

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QY      368 TAAGTGGCATCTGTAACCACTGTTGACAGTACACATGTCCTCCAGGTTGTTG 427
Db      364 TAAGTGGCATCTGTAACCACTGTTGACAGTACACATGTCCTCCAGGTTGTTG 423
QY      428 CTCCTTTACTGAGGTGTCTACGGATGGGGTCTTTGGGGTGTGGCTCATACAGAAAT 487
Db      424 CTCCTTTACTGAGGTGTCTACGGATGGGGTCTTTGGGGTGTGGCTCATACAGAAAT 483
QY      488 ATAGTGTCTACCTTTGTGACAGACACCTGTCAATCACTACATGATGACATCTT 547
Db      484 ATAGTGTCTACCTTTGTGACAGACACCTGTCAATCACTACATGATGACATCTT 543
QY      548 CCCCTTTTGAAGCTCTCTGCAACGGCTTTACATAAATGTCCTGATCTTTATTTGTT 607
Db      544 CCCCTTTTGAAGCTCTCTGCAACGGCTTTACATAAATGTCCTGATCTTTATTTGTT 603
QY      608 GTGACGCTGACATGGGGTCCCATGTTGCGGTTTAACTCTAATGTTTATTTCTT 667
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QY      668 TCCAGCATCTCCCGTTAGTTCTGCTAGAGGCGAGTCTAAAGCCTTCACTAGCTCAG 727
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QY      908 AGAAGCTTTTCAGAAATTAAGCTTTTCTGA 937
Db      904 AGAAGCTTTTCAGAAATTAAGCTTTTCTGA 933

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RESULT 2

AY405609 903 bp DNA linear GSS 16-DEC-2003
LOCUS
DEFINITION
Homo sapiens OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY405609
ACCESSION
AY405609
VERSION
AY405609.1 GI:39761583
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE

JOURNAL
Science 302 (5652), 1960-1963 (2003)

REFERENCE

Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Fertiera,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission

TITLE

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

COMMENT

FEATURES

1..903
/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN

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Best Local Similarity 80.6%; Pred. No. 4.9e-138;
Matches 728; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

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QY      95 CTAGGTTTCTACGCGGTGACGCTGTGGGAACTGGGCTTGATTAATCTGATAGGCTC 154
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QY      215 AGTTTCTTACAGACATATCCCAAAATGCTGATGAGTTTGTCTCAAGAGAAACATT 274
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RESULT 4
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LOCUS AY407110 799 bp DNA linear GSS 15-DEC-2003
 DEFINITION Pan troglodytes OR8B12 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY407110
 VERSION AY407110.1 GI:39763081
 KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 799)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Interfing nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 799)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

TITLE This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 COMMENT Location/Qualifiers
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 Best Local Similarity 83.0%; Pred. No. 6.5e-128;
 Matches 661; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 8 GCCGGAAGACTCTCTCGTACAGAGATTATCTCGAGGCTTATCCACAGCCCGGA 67
 Db 4 GCAGGCAAAACTCTCTGTGACAGAGTTATCTCGAAGCTTAAACCCACGCGGA 63
 QY 68 CTCACAGTCCCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 127
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 QY 128 CTGGGCTTATATCTGATAGAGGCTCACTCTCGCTGCATATCCCACTTTTTC 187
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 Db 304 TTTCT 363
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 DEFINITION Pan troglodytes OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY405610
 VERSION AY405610.1 GI:39761584
 KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 899)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Interfing nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 899)
 Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanendbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

TITLE This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 COMMENT Location/Qualifiers
 FEATURES
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QY 95 CTAGGCTTTCTAGCGGCTCAAGGTGTGGGGAACCTGGGCTTGAATACTGTAAGGCTC 154
DB 61 CTAGGCTTTCTAGCGGCTCAAGGTGTGGGGAACCTGGGCTTGAATACTGTAAGGCTC 120
QY 155 AACTCGGCTGATATCCCAATGTAATCTTTTCCCTCACTTGCCCTCGTAGATT 214
DB 121 AACNNTCAGNNCACACCCCTNNNNACNTCTTCTATACCTTGCTTCAATGATTT 180
QY 215 AGTTTCTAGACACATCAATTCCTCAAAATGCTGATGATGTTTGTCTCAAGAAACATT 274
DB 181 TGTATCTCANNNTTATCACTCCCAAAATGCTGATGATGTTTGTCTTAMNNNNACAC 240
QY 275 ATTCTCTGACAGGGGTATGAGTCACTCTTCTTCTGTTTCTTTCTTTCTGAG 334
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QY 875 CTGAGAAATAGAGTGTCAAACTGCGCTGAGAGAAACCTTTTCCAGAAATAGCTTTTC 933
DB 841 CTGAGAAATAGAGTGTCAAACTGCGCTGAGAGAAACCTTTTCCAGAAATAGCTTTTC 899

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RESULT 6
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LOCUS
DEFINITION
Mus musculus OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION
AY405611
VERSION
AY405611.1 GI:39761585
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 903)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,K.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
2 (bases 1 to 903)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J.,
Adams,M.D. and Cargill,K.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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QY 155 AACTCGGCTGATATCCCAATGTAATCTTTTCCCTCACTTGCCCTCGTAGATT 214
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QY 275 ATTCTCTGACAGGGGTATGAGTCACTCTTCTTCTGTTTCTTTCTTTCTGAG 334
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QY 335 TCCTTCATCTGTGCGGATGTGTGAGAGACCGCTACGTTGGAGCATCTGTAACCACTGTT 394
DB 301 TCTTTATCTGTGACCATGATGATGACCGGTATGTGCACTGTGTAACCCCTGATG 360
QY 395 TACAGATACCATATCTCTCCCGAGGTGTGTGCTCTTCTTCTGAGGTGTCTACAGGATG 454
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 DB 781 AAGGTCTCTCTTCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 875 CTGAGGATTAAGGATGTCAACTTGTCCCTGAAGAAACCTTTTCCAGAAATAGCTTTCT 934
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 QY 935 TGA 937
 DB 901 TGA 903

RESULT 7
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 DEFINITION AY405657
 ACCESSION AY405657.1 GI:35761631
 VERSION GSS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 930)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trics
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 930)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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OY		482	GGAATAATAGTGTTCCTACCTTTATGTGACAGAACACCCTGTCAATCACTACATNGTGTAC	541
Dd		478	GGAGGACATGCTGACACTTACTTTCTGTGATTCCAATATATATCCACCATTAATCTCTGTGA	537
OY		542	ATCCTTCCCCTTCTTGAAGCTCTCTGTGACAGGGCTCTTACATAAATGTCTGTGATCTTT	601
Dd		538	GTTCTTCCCCTTTTACAGCTCTCTGTGACACAGATCAATGCCAACAGAGCTTGTGTTTTT	597
OY		602	ATTGTTTGACCCGTGGATTTGGGAGTGGAGGCCATTTGGCCGTTTTATCTCTTAATGTTT	661
Dd		598	ATTGTTTGAGATGATCATCACAGCATCCAGCATCAGATCTTTATCTCTTAATGATTG	657
OY		662	ATCTTTTCCAGCATTCCTCCGGTTAGTTCTGTGAGGGCAGGTCTAAAGCTTTAGTAGC	721
Dd		658	ATTCTCTCCAACTTCTTAAGATTCCTTCTGTGATAGGTATGCCAAAGCTTTGGACACA	717
OY		722	TGAGCTCCTCATATAATTGACAGTTCTCTTTTCTTTGGGTCAGAGCTTTTACGTACCTC	781
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OY		782	AAACCCCTTCATTTTACCCCTGTGACAGGGGAGAAGTGTCTCCCTGTGTTATACACT	841
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DEFINITION			Genomic survey sequence.	
ACCESSION			AY419056	
VERSION			AY419056.1 GI:39775016	
KEYWORDS			GSS.	
SOURCE			Pan troglodytes (chimpanzee)	
ORGANISM			Pan troglodytes	
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.	
			1 (bases 1 to 930)	
			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	
			Todd,M.A., Tanendau,D.M., Civello,D.R., Lu,F., Murphy,B.,	
			Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Stansky,J.J.,	
			Adams,M.D. and Cargill,M.	
			Infering nonneutral evolution from human-chimp-mouse orthologous	
			gene trios	
TITLE			Science 302 (5652), 1960-1963 (2003)	
JOURNAL			14671302	
PUBLISHED			2 (bases 1 to 930)	
REFERENCES			Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	
AUTHORS			Todd,M.A., Tanendau,D.M., Civello,D.R., Lu,F., Murphy,B.,	
			Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Stansky,J.J.,	
			Adams,M.D. and Cargill,M.	
			Direct Submission	
TITLE			Submitted (16-NOV-2003) Celera Genomice, 45 West Gude Drive,	
JOURNAL			Rockville, MD 20850, USA	
COMMENT			These sequences were made by sequencing genomic exons and ordering	
			them based on alignment.	
FEATURES			Location/Qualifiers	
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Query Match 41.0%; Score 394.8; DB 29; Length 930;
Best Local Similarity 64.6%; Pred. No. 1.6e-83;
Matches 601; Conservative 0; Mismatches 327; Indels 3; Gaps 1;

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QY 2 ATGGGCGGAGAGACCTCTCCGAGAGAGTTATCTCCGAGGCTTATCCACAG 61
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DB 718 TGCAGCTCTCTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 777
QY 782 AAACCCCTTCCATTTTAAACCTGAGCCAGGAGAAAGTCTCTCTCTCTCTCT 841
DB 778 AAACCCCTTCCATTTTAAACCTGAGCCAGGAGAAAGTCTCTCTCTCTCTCT 837
QY 842 GTGGGCGCATGTTTAAACCATTAATCTACAGCTGAGGAAATAGAGATGCAAACTGCC 901
DB 838 GTAACTCCCATGTTGAATCCCTTATCTACAGCTGAGGAAATAGAGATGCAAACTGCC 897
QY 902 CTGAAGAACTTTTCTCAAGATTAAGCTTTT 932
DB 898 GTGCGAAGAAACGNNAGAGGCTAACTGTTT 928

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RESULT 10 AY419055

LOCUS 930 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens OR8A1 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION AY419055
VERSION AY419055.1 GI:39775015
KEYWORDS GSS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 930)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.D.,
Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)

REFERENCE PubMed 14671302
2 (bases 1 to 930)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.D.,
Adams,M.D. and Cargill,M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT These sequences were made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Location/Qualifiers
1..930

source
/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN

Query Match 40.7%; Score 391.8; DB 29; Length 930;
Best Local Similarity 64.6%; Pred. No. 8.3e-83;
Matches 601; Conservative 0; Mismatches 327; Indels 3; Gaps 1;

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QY 2 ATGGTGGCGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 61
DB 1 ATGGTGGCGAGAAATACCTCTACAGTACAGAGTTTCATTCAGAGTTTAAAGAGA 60
QY 62 CCGGAGCTCCAGCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 121
DB 61 GAGAGCTCCAGCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 122 GGAACCTGGGCTGATATCTCTGATAGGCTCACTCTCGCTGCATATCCCATGAC 181
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Db 361 GACCGCTAGTTGCGATCTGCCACCTTGTCTTACACATCATTAATGTCATGACACC 420
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 QY 842 GTGTGCTCCCTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 901
 Db 838 GTATCTCCCTGTTGATATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 897
 QY 902 CTGAAGAGAACTTTTCCAGATTAAGCTTTT 932
 Db 898 GTGCAAGAAACGCTGAGGGGTAAACTGTTT 928

RESULT 11 930 bp DNA linear GSS 17-DEC-2003
 AY419057
 LOCUS
 DEFINITION Mus musculus Oribal gene, VIRUAL TRANSCRIPT, partial sequence.
 ACCESSION AY419057
 VERSION AY419057.1 GI:39775017
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 930)
 REFERENCE 2 Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A.G., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
 2 (bases 1 to 930)
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.
 FEATURES
 SOURCE location/Qualifiers
 1..930
 /organism="Mus musculus"

ORIGIN
 Query Match 40.4%; Score 388.6; DB 29; Length 930;
 Best Local Similarity 64.3%; Pred. No. 4.8e-82;
 Matches 599; Conservative 0; Mismatches 329; Indels 3; Gaps 1;
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 /locus_tag="HCM6763"

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 Db 1 ATGCTGAGAGAAATCAATCAAGTACAGAGAGTTTCTCTGAGGCTTAATCACCAG 60
 QY 62 CCGGAGCTCAGAGTCCCGCT 121
 Db 61 CCGGAGCTCAGAGTCCCGCT 120
 QY 122 GGAAGCTGGCTGATATCTCTATAGGCTCACTCTGCGCTGATATCCCATGATAC 181
 Db 121 GGAAGCTGGCTGATATCTCTATAGGCTCACTCTGCGCTGATATCCCATGATAC 180
 QY 182 TTTTCCCTTCACTTCT 241
 Db 181 TTTTCCCTTCACTTCT 240
 QY 242 ATGCTGATGATTTTGTCTCAGAGAAACATTAATTTCTCTCAGAGGCTGATGATCAG 301
 Db 241 ATGCTGATGATTTTGTCTCAGAGAAACATTAATTTCTCTCAGAGGCTGATGATCAG 300
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 QY 842 GTGTGCTCCCTTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 901
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 QY 902 CTGAAGAGAACTTTTCCAGATTAAGCTTTT 932

Db 898 CTGGACAAACACTGAGAGAGAGCTCTTT 928

RESULT 12
CE158635 625 bp DNA linear GSS 25-SEP-2003
LOCUS CE158635
DEFINITION tigr-gss-dog-17000371402682 Dog Library Canis familiaris genomic,
genomic survey sequence.

ACCESSION CE158635
VERSION CE158635.1 GI:35286025
KEYWORDS GSS.
SOURCE
ORGANISM Canis familiaris (dog)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 625)
Kirkness, E.F., Balna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PubMed 14512627

COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirkness@tigr.org
Classes: Shotgun.
Location/Qualifiers

FEATURES
source
1..625
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/mol_type="genomic DNA"
/strain="Standard Poodle"
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/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

ORIGIN

Query Match 37.2%; Score 358.6; DB 29; Length 625;
Best Local Similarity 80.2%; Pred. No. 6.9e-75;
Matches 421; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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Db 401 TTTGCT 460
QY 380 TGTACCCACTGTTGTATACATGACATGATGATGATGATGATGATGATGATGATG 439
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QY 440 GGTGTCTACCGAGATGGGGGTTTTTGGGGCTGTGGCTATACAGAAATATAGTGTCTC 499
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RESULT 13
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LOCUS CB174479
DEFINITION OR_262RH1.020911.y1 Embryonic mouse olfactory epithelium library
Mus musculus cDNA clone ZOB1H11 5', mRNA sequence.

ACCESSION CB174479
VERSION CB174479.1 GI:37593108
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 748)
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A.,
Walker, M., Williams, E.M. and Trask, B.J.
Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and
unequal expression levels
Genome Biol. 4 (11), R71.1-R71.15 (2003)
Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98105-1024 USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org
Young gene new name GA_X6K02P2PVD-32156773-32157705
Young gene old name GA_X5JB7W60MJ-114653-1145421
Zhang gene name MOR167-3
Seq primer: M13 Reverse

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/clone="ZOB1H11"
/issue_type="Olfactory and respiratory epithelium"
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LambdaZAP11-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Tyler Cutforth. mRNA was prepared from the
olfactory and respiratory epithelium of mixed
Swiss-Webster and C57BL/6 embryos, aged E16.5-E18.5.
Oligo-dT primed cDNA was directionally cloned into
Stratagene's LambdaZAP11-XR vector."

ORIGIN

Query Match 36.4%; Score 350.6; DB 14; Length 748;
Best Local Similarity 69.8%; Pred. No. 5.7e-73;
Matches 473; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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QY 297 GTCAATCT 356
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Db	121	CTTATGATCGCTATGTGGCCATCTGTATCCAGCTCTTTGATACGGTTGCCATGTCCCTTA	180
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Db	241	ACACAGGATGCAGNCTGAGACTGACCTTCTGTGATGCTCAACCACTCAACCACTCTTCT	300
Qy	537	GTGACATCCTTCCCTTCTTGAAGCTCTCCGTGCAAGGGCTCTTACATAAATGTCTGTGTA	596
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Qy	777	ACCTCAAAACCCCTTCCATTTTACCCTCGGAGACAGAGGAAAGTGCCTCCCTGTCTATA	836
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RESULT 14

AZ255734

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ255734 726 bp DNA linear GSS 26-JUL-2000

RPCL-23-16619. TJ RPCL-23 Mus musculus genomic clone RPCL-23-16619,

genomic survey sequence.

AZ255734

AZ255734.1 GI:9458784

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 726)

Zhao,S., Nierman,W., Feidblyum,T., Malek,J., Shatsman,S.,

Akhter,B., Levins,M., McGarrn,S., Tsegaye,G., Geer,K., Krol,M., de

Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCL-23

Unpublished (1999)

Other GSSs: RPCL-23-16619.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@ligr.org

Clones are derived from the mouse BAC library RPCL-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACRA Resources (<http://bacres.med.buffalo.edu/orderingframe.htm>)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.ligr.org/cdb/bac_ends/mouse/bac_end_intro.html

plate: 166 row: I column: 9

FEATURES	Source	Location/Qualifiers
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		/sex="Female"
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		/clone_id="RP11-23"
		/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN		
Query Match	36.4%; Score 350.2; DB 28; Length 726;	
Best Local Similarity	67.8%; Pred. No. 7.1e-73;	
Matches 490; Conservative	0; Mismatches 233; Indels 0; Gaps 0;	
Db	75	TCGCCGCTTCTTCCTGTTTCTAGATTCTACGCGGTACGGGTGAGGAGACCTGGCT 134
QY	3	TCCCTCGTCTTCTTGTCTCTGTATGTATAGTAACTAGACCGGGAATTTGGGT 62
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QY	123	ACTGTCTTTGATAGACCTCTGTTACTTTCAGTGTTCACCCAAATGCTGTGAAGT 182
Db	255	TTGTCTCAGGAGAACATTTATTCCTTACAGGGGTGTATGATGATCTTCTTCTCT 314
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Db	315	GTTCTCTTGTCTTCTGAGTCTTCAATCCGTGGGGATGTGAGAGCCGCTACGAG 374
QY	243	CATCTTTTGTATTTCTGAGTGTATGTATGTCAATGAGCTATGATGCTATGAG 302
Db	375	GCATCTGTAAACCACTGTGTACACGATACACATGTCTCCCAAGTGTGTCTCTT 434
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QY	363	TGCTTGTGTTCACTTGTATGATGATTTCTGTGGTGCATGAGCTCAACAGAGTATG 422
Db	495	TTCTACCTTTTGTGACAGACCACTTGTCAATCACTACATGTGTGACATCCTTCC 554
QY	423	GATGACCTTGTGTGATGACAAACCAATCAATCACTACTTGTGTGACATCTCTCG 482
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Db	735	TAATTCAGTTCTCTTTCTTTGGGTGAGAGGTTTATAGTACTCAAAACCCCTTCA 794
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QY 795 TTT 797
Db 723 TTT 725

RESULT 15
BZ281255
LOCUS BZ281255 848 bp DNA linear GSS 15-OCT-2002
DEFINITION CH230-344K8, TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION BZ281255
VERSION BZ281255.1 GI:24006451
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 848)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shivartebyan, A., Gebregiorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-344K8.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ordering information.htm). BAC end
plate: http://www.tigr.org/tcdb/bac_ends/rat/bac_end_intro.html
Plate: 344 row: K column: 8
Seq primer: 17
Class: BAC ends.
Location/Qualifiers
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/clone_lib="CHORI-230 Segment 2"
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CHORI-230 Rat (BN/SNHsd/MCM) BAC library produced by
Pieter de Jong"

ORIGIN
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Best Local Similarity 68.1%; Pred. No. 8.2e-69;
Matches 492; Conservative 0; Mismatches 228; Indels 2; Gaps 2;

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Db 1 TCTCGATATCTACTGTCTCCTCCAAAATGCTATGAACTTTAATGTGAGCAAGAA 60
QY 271 CATATTTCTCTACAGGGGTATGAGTCTTCTTCTCTCTGTTCTTTGCTTTTC 330
Db 61 TGCATTTTCTTACATGGAGTGTGACCAAGCTATATTCTTTGTTTGTGCAATTC 120
QY 331 TGAAGCTCTTCACTCTGTGGCGATGTGAGAGCCGCTACCTGGGCACTGTAAACCACT 390
Db 121 TGAAGTTATGTGTGACTTCAATGGCTTATGATGCGCTTGTGGCACTCTTAATCCACT 180
QY 391 GTTGACAGATCAACATGCTCTCCCAAGGTGTGTTGCTCTTTACTGGGATGCTACGG 450

Db 181 TTTGTACACTGTGGCCATGCTCCCTAAATGTGTGAACTTATGCTTGAGCAATATT 240
QY 451 GATGGGGGTTTTGGGGGCTGTGGCTCATACAGAAATATAGTTTCTACCTTTTGGC 510
Db 241 AATGCAATTTCTGTGGCCATGCTCACAGAGATGTATGTAAGACTGACCTTCTGTA 300
QY 511 AGACAACCTTGATCAATCACTACATGTGTGACATCTTCCCTTCTGTGAGCTCTCTGCA 570
Db 301 TGTACACACATCAACATTAATCTGTGTGACATCTTCCCTGTGATGACAGCTCTCATGAC 360
QY 571 CGGCTCTCAATAAAGTCTGTCATCTTTATGTGTGACGCTTGCGATGGGATGGCG 630
Db 361 CAGACCTTATGTCAATGAATGTGTGATTTCAATGTGTGAGGACATCAATATTGTGCT 420
QY 631 CATTTGCGCTTTTATCTTATGTTTATGTTTATCTTTCACATCTTCCGCTAGTTC 690
Db 421 CAGATCAACATTTTATCTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 480
QY 691 TGTGAGGCGAGGTCTTAAAGCTTCAATGCTGAGCTTCTTCAATATTTGCAAGTTTCT 750
Db 481 TAATGAAGGCAAGTCCAAAGCTTCAAGCACTGCAAGTCCAAATATTTGCAAGTTTCT 540
QY 751 TTTCTTGGGTGAGAGCTTTTACGTTTACGTTTACGTTTACGTTTACGTTTACGTTTAC 810
Db 541 GTTCTTGTGATCAGTGCAATTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATG 600
QY 811 GGGGAAGTGTCT 870
Db 601 AGAAAAAACCTTCTGTTATTTTATTAACCAATGTGTGTTCTTATGATGAATTC-TTATCTTA 659
QY 871 CAGCTGAGGAATTAAGATGTCAAACTGGCCTGAAGAACTTTTCCAGATTAAGCTT 930
Db 660 CAG-TTAAAGGACAAAGATGTAAATAATGGCCTGAAGAACTTTGAGTAAAGCAATT 718
QY 931 TT 932
Db 719 TT 720

Search completed: September 30, 2004, 01:22:32
Job time : 3090 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 01:24:18 ; Search time 4162 Seconds

(without alignments)
10028.674 Million cell updates/sec

Title: US-10-023-597-23

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Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 20

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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41: em_hvg_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	963	100.0	963	AX555964	AX555964 Sequence
2	912	94.7	17291	AC083958	AC083958 Homo sapi
3	912	94.7	192926	AP000916	AP000916 Homo sapi
4	911	94.6	994	AX241500	AX241500 Sequence
5	706	73.3	931	AX646877	AX646877 Sequence
6	289	30.0	667	AY448475	AY448475 Gorilla g
7	224	23.3	485	AR427386	AR427386 Sequence
8	224	23.3	485	BD122939	BD122939 EST and e
9	133	13.8	668	AY448357	AY448357 Hylobates
10	121	12.6	886	AX646875	AX646875 Sequence
11	121	12.6	935	AX241493	AX241493 Sequence
12	121	12.6	886	AX448924	AX448924 Cercopit
13	77	8.0	667	AY449293	AY449293 Saimiri s
14	67	7.0	668	AY448835	AY448836 Callithr
15	57	5.9	487	AX181578	AX181578 Sequence
16	57	5.9	487	AF179842	AF179842 Saimiri b
17	53	5.5	667	AY448503	AY448503 Alouatta
18	53	5.5	667	AY448759	AY448759 Cercocebu
19	43	4.5	661	SCO233799	AJ233799 Stenella
20	41	4.3	258873	AC096935	AC096935 Rattus no
21	39	4.0	486	AX181571	AX181571 Sequence
22	39	4.0	486	AF179838	AF179838 Saimiri b
23	39	4.0	487	AX181511	AX181511 Sequence
24	39	4.0	487	AX181560	AX181560 Sequence
25	39	4.0	487	AF179805	AF179805 Callithr
26	39	4.0	487	AF179832	AF179832 Saimiri s
27	39	4.0	489	AX181491	AX181491 Sequence
28	39	4.0	489	AF179793	AF179793 Macaca sy
29	39	4.0	491	AX181525	AX181525 Sequence
30	39	4.0	491	AF179812	AF179812 Pongo pyg
31	39	4.0	491	AF399511	AF399511 Homo sapi
32	39	4.0	667	AY449228	AY449228 Ateles fu
33	39	4.0	667	AY448895	AY448895 Cercopit
34	39	4.0	675	AX242246	AX242246 Sequence
35	39	4.0	930	AX242246	AX242246 Sequence
36	39	4.0	933	AX244609	AX244609 Sequence
37	39	4.0	933	AX448443	AX448443 Sequence
38	39	4.0	933	BD144473	BD144473 Novel G-P
39	39	4.0	953	AX554459	AX554459 Sequence
40	39	4.0	976	AX556206	AX556206 Sequence
41	39	4.0	991	AX702842	AX702842 Sequence
42	39	4.0	1333	AX646099	AX646099 Sequence
43	39	4.0	1333	AB065834	AB065834 Homo sapi
44	39	4.0	1655	AX357037	AX357037 Sequence
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ALIGNMENTS

RESULT 1
AX555964 963 bp DNA linear PAT 27-NOV-2002
LOCUS AX555964
DEFINITION Sequence 23 from Patent WO0250275.
ACCESSION AX555964
VERSION AX555964.1 GI:25899399
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
Padigaru, M., Kekuda, R., Li, L., Ballinger, R.A., Casman, S.J.,
Spytek, K.A., Baumgartner, J.C. and Burgess, C.B.
Novel proteins and nucleic acids encoding same

JOURNAL Submitted (17-DEC-1999) Maahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22, Sphulho-Chou, Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.go.jp, URL: <http://hsp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENTS On Jan 31, 2003 this sequence version replaced gi:15637083.
LOCATION/Qualifiers

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ORIGIN /clone="RP11-728D14"
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ORIGIN

Query Match	94.6%	Score 911;	DB 6;	Length 994;
Best Local Similarity	99.98%	Pred. No. 0;		
Matches 961;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

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VVKALKRTERSRFS"

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[illegible]

TITLE
Loss of olfactory receptor genes coupled with the acquisition of full trichromatic vision in primates

JOURNAL
Unpublished

REFERENCE
2 (bases 1 to 667)

AUTHORS
Gillad, Y., Wiebe, V., Przeworski, M., Lancel, D. and Paabo, S.

TITLE
Submitted (20-OCT-2003) Max Plank Institute for Evolutionary Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

JOURNAL
Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES
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/gene="olfactory receptor-like protein"

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Best Local Similarity 100.0%; Pred. No. 1.2e-147; Indels 0; Gaps 0;
Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 431 CTTTACTGGGTGTCTACGGATGGGGTTTGGGGCTGCTCATACAGAAATXA 490
DB 242 CTTTACTGGGTGTCTACGGATGGGGTTTGGGGCTGCTCATACAGAAATATA 301
QY 491 GTGTTTCACCTTTTGGGACAGACCTTGTCATCTCATGTGTGACATCTTCCC 550
DB 302 GTGTTTCACCTTTTGGGACAGACCTTGTCATCTCATGTGTGACATCTTCCC 361
QY 551 CTTCTTGAAGCTCTCTGACAGAGCTCTTACATAATGCTGTCATCTTATTTGTTG 610
DB 362 CTTCTTGAAGCTCTCTGACAGAGCTCTTACATAATGCTGTCATCTTATTTGTTG 421
QY 611 ACCGTTGGCATTTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATCTTCC 670
DB 422 ACCGTTGGCATTTGGGGTCCCATTTGTCCTTTTATCTTATGTTTATCTTCC 481
QY 671 AGCATTTCTCCGCTAGTTCTGTGAGGAGGAGTCTAAAGCTTCAGTA 719
DB 482 AGCATTTCTCCGCTAGTTCTGTGAGGAGGAGTCTAAAGCTTCAGTA 530

RESULT 7
AR427386/c 485 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION
Sequence 18883 from patent US 6639063.
ACCESSION
AR427386
VERSION
AR427386.1 GI:40182496
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 485)
AUTHORS
Edwards, J.-B.D.M., Robert, S. and Giordano, J.-Y.
TITLE
EST's and encoded human proteins
JOURNAL
Patent: US 6639063-A 18883 28-OCT-2003;
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QY 402 TCACCATGCTCCCGAGGTGTGTTGCTCTTTTACTGGGTCTTACGGATGGGGTTT 461
DB 265 TCACCATGCTCCCGAGGTGTGTTGCTCTTTTACTGGGTCTTACGGATGGGGTTT 206

QY 462 TTGGGGCTGTGCTCATACAGAAATATAGTTTCTACCTTTTGGACAGACCTTG 521
DB 205 TTGGGGCTGTGCTCATACAGAAATATAGTTTCTACCTTTTGGACAGACCTTG 146
QY 522 TCATCTCATGTGTGGAATCTCTTCCCTTTTGAAGCTCTCTGCAAGGCTTTACA 581
DB 145 TCATCTCATGTGTGGAATCTCTTCCCTTTTGAAGCTCTCTGCAAGGCTTTACA 86
QY 582 TAAATGCTGTGCTCATCTTATTTGTTGTGACCGTTGGCATTTGG 625
DB 85 TAAATGCTGTGCTCATCTTATTTGTTGTGACCGTTGGCATTTGG 42

RESULT 8
BD12293/c 485 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION
EST and encoded human protein.
ACCESSION
BD12293
VERSION
BD12293.1 GI:23217884
KEYWORDS
UP 2002010789-A/15016.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
1 (bases 1 to 485)
AUTHORS
Edwards, J.B.D.M., Robert, S. and Giordano, J.E.
TITLE
EST and encoded human protein
JOURNAL
Patent: JP 2002010789-A 15016 15-JAN-2002;
COMMENT
GENEST CORP
OS Homo sapiens (human)
PN JP 2002010789-A/15016
PD 15-JAN-2002
PF 07-AUG-2000 JP 2002080989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
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FT source
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DB 145 TCATCTCATGTGTGGAATCTCTTCCCTTTTGAAGCTCTCTGCAAGGCTTTACA 86
QY 582 TAAATGCTGTGCTCATCTTATTTGTTGTGACCGTTGGCATTTGG 625
DB 85 TAAATGCTGTGCTCATCTTATTTGTTGTGACCGTTGGCATTTGG 42

RESULT 9

AY448357 668 bp DNA linear PRI 07-DEC-2003
 LOCUS Hylobates syndactylus clone OLG_29 olfactory receptor-like protein
 DEFINITION
 ACCESSION AY448357
 VERSION AY448357.1 GI:38634385
 KEYWORDS
 SOURCE Hylobates syndactylus (slamang)
 ORGANISM Hylobates syndactylus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hyloteriidae; Hylobates.
 1 (bases 1 to 668)
 Giled,Y., Wiebe,Y., Przeworski,M., Lancel,D. and Paabo,S.
 Loss of olfactory receptor genes coupled with the acquisition of
 full trichromatic vision in primates
 full trichromatic vision in primates
 Unpublished
 JOURNAL
 REFERENCE
 AUTHORS Giled,Y., Wiebe,Y., Przeworski,M., Lancel,D. and Paabo,S.
 TITLE Direct Submission
 JOURNAL Submitted (20-OCT-2003) Max Planck Institute for Evolutionary
 Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
 Location/Qualifiers
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ORIGIN
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 Best Local Similarity 100.0%; Pred.No. 1.9e-61;
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QY 482 GGAATATGATGTTCTTCTGACCTTTTGTGACGACACCTGTCATCTACATCTGATC 541
 DB 293 GGAATATGATGTTCTTCTGACCTTTTGTGACGACACCTGTCATCTACATCTGATC 352
 QY 542 ATCTTCCCTCTTGTGAGCTCTCTGCAACGCTCTTACATTAATGCTCTGTCATCTTT 601
 DB 353 ATCTTCCCTCTTGTGAGCTCTCTGCAACGCTCTTACATTAATGCTCTGTCATCTTT 412
 QY 602 ATTGTTGTGACCG 614
 DB 413 ATTGTTGTGACCG 425

RESULT 10
 AX646875 886 bp DNA linear PAT 04-MAR-2003
 LOCUS Sequence 1067 from Patent EP1270724.
 DEFINITION AX646875
 ACCESSION AX646875.1 GI:28799398
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1
 Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
 Guanine triphosphate-binding protein coupled receptors
 Patent: EP 1270724-A, 1067 02-JUN-2003;
 National Institute of Advanced Science and Technology Incubation, Ltd.
 (JP)
 Location/Qualifiers
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FEATURES
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 Best Local Similarity 100.0%; Pred.No. 8.2e-55;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CTCTCTCTGTTCTAGATTCTACGGGCTACGGGTGGGGAACCTGGGCTTGATAT 141
 DB 281 CTCTCTCTGTTCTAGATTCTACGGGCTACGGGTGGGGAACCTGGGCTTGATAT 340
 QY 142 CCGATAGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 201
 DB 341 CCGATAGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 400
 QY 202 C 202
 DB 401 C 401

RESULT 11
 AX241493 935 bp DNA linear PAT 26-SEP-2001
 LOCUS Sequence 241 from Patent WO0127158.
 DEFINITION AX241493
 ACCESSION AX241493.1 GI:15798368
 VERSION
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE
 1 Bellenson,J., Smith,D., Lancel,D., Glusman,G., Fuchs,T. and
 Yanai,I.
 TITLE Olfactory receptor sequences
 JOURNAL Patent: WO 0127158-A, 241 19-APR-2001;
 Disiscenes (US) ; YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
 Location/Qualifiers
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ORIGIN
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 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 CTCTCTCTGTTCTAGATTCTACGGGCTACGGGTGGGGAACCTGGGCTTGATAT 141
 DB 81 CTCTCTCTGTTCTAGATTCTACGGGCTACGGGTGGGGAACCTGGGCTTGATAT 140
 QY 142 CCGATAGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 201
 DB 141 CCGATAGGGCTCACTCTGCGCTGCATATCCCATGACTTTTCCCTTCAACTGTC 200
 QY 202 C 202
 DB 201 C 201

RESULT 12
 AY448924 667 bp DNA linear PRI 07-DEC-2003
 LOCUS

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DEFINITION Cercopithecus aethiops clone OLG_7 olfactory receptor-like protein
ACCESSION AY448924
VERSION AY448924.1 GI:38634952
KEYWORDS
SOURCE
ORGANISM
    Cercopithecus aethiops (African green monkey)
REFERENCE
    Cercopithecus aethiops
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
    Cercopithecinae; Cercopithecus.
AUTHORS
    Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE
    Loss of olfactory receptor genes coupled with the acquisition of
    full trichromatic vision in primates
JOURNAL
    Unpublished
REFERENCE
    2 (bases 1 to 667)
AUTHORS
    Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE
    Direct Submission
JOURNAL
    Submitted (20-OCT-2003) Max Plank Institute for Evolutionary
    Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
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QY 491 GTGTTTCACCTTTGTGACAGACACTTGTCAATCACTGATGTCATCCTTCCC 550
DB 302 GTGTTTCACCTTTGTGACAGACACTTGTCAATCACTGATGTCATCCTTCCC 361
QY 551 CTCTTGAGCTCTCCTG 567
DB 362 CTCTTGAGCTCTCCTG 378

RESULT 13
LOCUS AY449293 667 bp DNA linear PRI 07-DEC-2003
DEFINITION Saimiri sciureus clone OLG_66 olfactory receptor-like protein gene,
    partial sequence.
ACCESSION AY449293
VERSION AY449293.1 GI:38635321
KEYWORDS
SOURCE
    Saimiri sciureus (common squirrel monkey)
    Saimiri sciureus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
    Saimiri.
REFERENCE
    1 (bases 1 to 667)
AUTHORS
    Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE
    Loss of olfactory receptor genes coupled with the acquisition of
    full trichromatic vision in primates
JOURNAL
    Unpublished
REFERENCE
    2 (bases 1 to 667)
AUTHORS
    Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE
    Direct Submission
JOURNAL
    Submitted (20-OCT-2003) Max Plank Institute for Evolutionary
    Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
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QY 491 GTGTTTCACCTTTGTGACAGACACTTGTCAATCACTGATGTCATCCTTCCC 550
DB 302 GTGTTTCACCTTTGTGACAGACACTTGTCAATCACTGATGTCATCCTTCCC 361
QY 551 CTCTTGAGCTCTCCTG 567
DB 362 CTCTTGAGCTCTCCTG 378

RESULT 14
LOCUS AY448836 668 bp DNA linear PRI 07-DEC-2003
DEFINITION Callithrix jacchus clone OLG_58 olfactory receptor-like protein
    gene, partial sequence.
ACCESSION AY448836
VERSION AY448836.1 GI:38634864
KEYWORDS
SOURCE
    Callithrix jacchus (white-tufted-ear marmoset)
    Callithrix jacchus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
    Callitrix.
REFERENCE
    1 (bases 1 to 668)
AUTHORS
    Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE
    Loss of olfactory receptor genes coupled with the acquisition of
    full trichromatic vision in primates
JOURNAL
    Unpublished
REFERENCE
    2 (bases 1 to 668)
AUTHORS
    Gild, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.
TITLE
    Direct Submission
JOURNAL
    Submitted (20-OCT-2003) Max Plank Institute for Evolutionary
    Anthropology, Deutscher Platz 6, Leipzig 04103, Germany
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        /clone="OLG 58"
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        Primate Center in Goettingen, Germany"
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QY 290 TGTATGA 296
DB 101 TGTATGA 107

RESULT 15
LOCUS AX181578 487 bp DNA linear PAT 07-AUG-2001
DEFINITION Sequence 366 from Patent WO0146262.
ACCESSION AX181578

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VERSION AX181578.1 GI:15141666
 KEYWORDS
 SOURCE
 ORGANISM

Saimiri boliviensis (Bolivian squirrel monkey)
 Saimiri boliviensis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
 Saimiri.

REFERENCE
 1 Rouquier, S. and Giorgi, D.
 Olfactory receptor genes and pseudogenes in primates and mouse
 Patent: WO 0146262-A 366 28-JUN-2001;
 JOURNAL CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)

FEATURES
 source location/Qualifiers

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 NF"

ORIGIN

Query Match 5.9%; Score 57; DB 6; length 487;
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 |||||

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 Job time : 4167 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments) cell updates/sec

8685.806 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963

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Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 20

Total number of hits satisfying chosen parameters: 151

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	660	68.5	960	9 ADC86616	ADC86616 Human GPC
5	121	12.6	986	9 ADC86614	ADC86614 Human GPC
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8	39	4.0	486	4 AAH84095	AAH84095 Mouse olf
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26	33	3.4	486	4 AAH84022	Aah84022 Eulemar f
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36	35	2.9	945	9 AAD12820	Aad12820 cDNA enco
37	36	2.9	950	6 AAF88458	Aaf88458 Human GPC
38	37	2.9	950	6 AAD12838	Aad12838 cDNA enco
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41	40	2.7	939	4 AAH31803	Aah31803 Human olf
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ALIGNMENTS

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ID	AAF88413
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AC	AAF88413;
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DT	12-NOV-2002 (first entry)
XX	
DE	Human GPCRX cDNA SEQ ID 23.
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KW	Human; anti-HIV; nootropic; antistatic; antiarteriosclerotic; GPCRX;
KW	immunomodulatory; cytosolic; antiinflammatory; AROS;
KW	antidiabetic; neuroprotective; anorectic; haemostatic; antibacterial;
KW	fungicide; protozoal; virucide; human G-protein coupled receptor;
KW	gene therapy; vaccine; cardiomyopathy; atherosclerosis; diabetes;
KW	cell signal processing; cancer; obesity; neurodegenerative disorder;
KW	cachexia; anorexia; Alzheimer's disease; Parkinson's disease;
KW	immune disorder; graft versus host disease; bronchial asthma;
KW	Crohn's disease; multiple sclerosis; haemophilia; infectious disease;
KW	idiopathic thrombocytopenic purpura; gene; ss.
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OS	Homo sapiens.
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PN	WO200250275-A2.
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PD	27-JUN-2002.
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18-DEC-2001;	2001WC-US048958.
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18-DEC-2000;	2000US-0256635P.
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21-DEC-2000;	2000US-0257876P.
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04-JAN-2001;	2001US-0259743P.
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16-AUG-2001;	2001US-0312902P.
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(CURA-)	CURAGEN CORP.
XX	

1. *Introduction*
 2. *Background*
 3. *Methods*
 4. *Results*
 5. *Discussion*
 6. *Conclusion*
 7. *Acknowledgments*
 8. *References*
 9. *Appendix*
 10. *Supplementary Materials*
 11. *Tables*
 12. *Figures*
 13. *Tables*
 14. *Figures*
 15. *Tables*
 16. *Figures*
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 99. *Tables*
 100. *Figures*

Belenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I.

[illegible]

DR WPI; 2001-290713/30.
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 XX
 XX Claim 8; Page 276; 1857pp; English.
 XX
 CC The present sequence is one of a number of isolated polynucleotides which
 CC encode polypeptides involved in olfactory sensation. The polynucleotides
 CC can be used in screening for olfactory agonists and antagonists. The
 CC methods allow for the determination of primary scents and the
 CC identification of the odor receptors used to detect these primary
 CC scents. The methods also enable determination of secondary scents and the
 CC identification of combinations of odor receptors that are involved in
 CC detecting such secondary scents. This enables the construction of a scent
 CC representation (also called a scent fingerprint or scent profile), which
 CC may be used to re-create and edit scents. Libraries of olfactory
 CC receptors are useful for determining the interaction pattern of a
 CC composition with the receptors, and can be used for determining
 CC differences in the olfactory faculties of different individuals
 CC
 XX Sequence 994 BP; 201 A; 250 C; 207 G; 336 T; 0 U; 0 Other;
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 Matches 961; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 121 GGGAACTGGGCTTGAATCCGATAGAGGCTCACTCGGCTGATATCCCATGTAC 180
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 DB 961 GA 962

RESULT 3

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 XX 01-JAN-2004 (first entry)
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 KW ds; gene; human; GPCR;
 KW Guanosine triphosphate-binding protein coupled receptor; gene therapy.
 OS Homo sapiens.
 XX
 XX BP1270724-A2.
 XX
 XX 02-JAN-2003.
 PD
 XX
 XX 18-JUN-2002; 2002EP-00013517.
 PF
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 XX 18-JUN-2001; 2001JP-00246789.
 PR
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 XX (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 XX
 XX Suwa M, Aseai K, Akiyama Y, Aburatani H;
 XX
 DR WPI; 2003-315783/31.
 DR P-PSDB; ADCS6617.
 PT New polynucleotide, useful for preparing a composition for treating a
 PT patient in need of increased or suppressed activity or expression of the
 PT guanosine triphosphate-binding protein coupled receptor.
 XX
 XX Claim 1; SEQ ID NO 1069; 28bp; English.
 PS
 XX The invention relates to a novel polynucleotide encoding a guanosine
 XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
 XX the invention may have a use in gene therapy. The polynucleotide and
 XX polypeptide are useful for preparing a composition for treating a patient
 XX in need of increased or suppressed activity or expression of the
 XX guanosine triphosphate-binding protein coupled receptor. The
 XX polynucleotide sequences shown in ADCS5548-ADCS7616 encode GPCR's of the
 CC invention.
 CC
 CC Sequence 931 BP; 202 A; 215 C; 180 G; 334 T; 0 U; 0 Other;
 SQ
 Query Match 73.3%; Score 706; DB 9; Length 931;
 Best Local Similarity 99.9%; Pred. No. 0;


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Db      61 GCCGGAGCTCCAGTCCCGTCTTCTCTCTAGTTCCTACGCGGTACAGTGGT 120
QY      121 GGGGAACTGGGCTGATATATCTGATAGGCGTCACTCGCTGCAATATCCCATGA 180
Db      121 GGGGAACTGGGCTGATATATCTGATAGGCGTCACTCGCTGCAATATCCCATGA 180
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Db      538 CATCTCTCCCTCTTCTGAGTCTCTCCGCAAGCGCTCTTCAATATGCTGATGATCT 597
QY      601 TATGTTGTGACCGTGTGATGGGCTGCGCAATGTTGCGCTTTTATCTTATGATG 660
Db      598 TATGTTGTGACCGTGTGATGGGCTGCGCAATGTTGCGCTTTTATCTTATGATG 657
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Db      658 TATCTCTTCCAGATTTCTCGCGGTAGTCTGTGAGGCAAGCTTAAAGCTTCAGTGA 717
QY      721 CTGCACTCTCAATATGATGATGATCTCTTCTTCTTGGGTGAGGCTTTTACGATCT 780
Db      718 CTGCACTCTCAATATGATGATGATCTCTTCTTCTTGGGTGAGGCTTTTACGATCT 777
QY      781 CAAGCCCTCTTCAATTTTACCTCTGAGCAAGGGAAGTCTCTCTCTTCTTATACAC 840
Db      778 CAAGCCCTCTTCAATTTTACCTCTGAGCAAGGGAAGTCTCTCTCTTCTTATACAC 837
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QY      901 CTTGAAGAGAACCTTTTCCAGAAATAGCTTTTCTTGAATAAATTTTGAACAAG 960
Db      898 CTTGAAGAGAACCTTTTCCAGAAATAGCTTTTCTTGAATAAATTTTGAACAAG 957
QY      961 AGA 963
Db      958 AGA 960

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RESULT 5
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ID ADCC8614 standard; DNA; 886 BP.
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AC ADCC8614;

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XX      01-JAN-2004 (first entry)
DT
XX      Human GPCR gene SEQ ID NO:1067.
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XX      ds; gene; human; GPCR;
XX      guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX      Homo sapiens.
XX      EPI270724-A2.
XX      02-JAN-2003.
XX      18-JUN-2002; 2002EP-00013517.
XX      18-JUN-2001; 2001JP-00246789.
XX      (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX      (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX      Suwa M, Asai K, Akiyama Y, Aburatani H;
XX      WPI; 2003-315783/31.
XX      P-PSDB; ADCC8615.
XX      New polynucleotide, useful for preparing a composition for treating a
XX      patient in need of increased or suppressed activity or expression of the
XX      guanosine triphosphate-binding protein coupled receptor.
XX      Claim 1; SEQ ID NO 1067; 28pp; English.
XX
XX      The invention relates to a novel polynucleotide encoding a guanosine
XX      triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX      the invention may have a use in gene therapy. The polynucleotide and
XX      polypeptide are useful for preparing a composition for treating a patient
XX      in need of increased or suppressed activity or expression of the
XX      guanosine triphosphate-binding protein coupled receptor. The
XX      polynucleotide sequences shown in ADCC8548-ADCC87616 encode GPCR's of the
XX      invention.
XX
XX      Sequence 886 BP; 168 A; 233 C; 176 G; 309 T; 0 U; 0 Other;
XX
XX      Query Match      12.6%; Score 121; DB 9; Length 886;
XX      Best Local Similarity 100.0%; Pred. No. 3.1e-50;
XX      Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      82 CTTCTCTCTGTTCTAGATTCTACGCGGTACAGGCTGATGGGGAACCTGAGTATAT 141
Db      281 CTTCTCTCTGTTCTAGATTCTACGCGGTACAGGCTGATGGGGAACCTGAGTATAT 340
QY      142 CTTGATAGGCTCAACTCTGCTGCAATATCCCATGACTTTTCCCTTTCAACTGTG 201
Db      341 CTTGATAGGCTCAACTCTGCTGCAATATCCCATGACTTTTCCCTTTCAACTGTG 400
QY      202 C 202
Db      401 C 401

```

RESULT 6
AAH31668
ID AAH31668 standard; DNA; 935 BP.
XX
AC AAH31668;
XX
XX 30-JUN-2001 (first entry)
XX
XX Human olfactory receptor polynucleotide, SEQ ID NO: 241.
XX
XX Human olfactory receptor; OR; primary scent determination;
XX
XX secondary scent determination; polypeptide library; odour receptor;
XX
XX scent profile; scent fingerprint; scent representation; ds.
XX

```

XX OS Homo sapiens.
XX PN WO200127158-A2.
XX PD 19-APR-2001.
XX XX
XX PF 06-OCT-2000; 2000WO-US027582.
XX PR 08-OCT-1999; 99US-0158615P.
XX PR 24-FEB-2000; 2000US-0184809P.
XX XX
XX PA (DIGI-) DIGISCENTS.
XX PA (YEDA) YEDA RES & DEV CO LTD.
XX PI Belleson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX DR WPI; 2001-290713/30.
XX XX
XX PT New polynucleotides which encode polypeptides involved in olfactory
XX PT sensation for identifying olfactory agonists and antagonists.
XX PS Claim 8; Page 273; 1857pp; English.
XX XX
XX CC The present sequence is one of a number of isolated polynucleotides which
XX CC encode polypeptides involved in olfactory sensation. The polynucleotides
XX CC can be used in screening for olfactory agonists and antagonists. The
XX CC methods allow for the determination of primary scents and the
XX CC identification of the odour receptors used to detect these primary
XX CC scents. The methods also enable determination of secondary scents and the
XX CC identification of combinations of odour receptors that are involved in
XX CC detecting such secondary scents. This enables the construction of a scent
XX CC representation (also called a scent fingerprint or scent profile), which
XX CC may be used to re-create and edit scents. Libraries of olfactory
XX CC receptors are useful for determining the interaction pattern of a
XX CC composition with the receptors, and can be used for determining
XX CC differences in the olfactory faculties of different individuals
XX SQ
SQ Sequence 935 BP; 189 A; 238 C; 190 G; 318 T; 0 U; 0 Other;
Query Match 12.6%; Score 121; DB 4; Length 935;
Best Local Similarity 100.0%; Pred. No. 3.1e-50;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82 CTTCTTCTGTTTCTAGGTTTCTACGGGTCACGGTGTGGGAACTGGGCTTGATAT 141
DB 81 CTTCTTCTGTTTCTAGGTTTCTACGGGTCACGGTGTGGGAACTGGGCTTGATAT 140
QY 142 CCGTAGGGCTCAACTCTCGCGTCGATATCCCATGACTTTTCCGCTTCAACTGTC 201
DB 141 CCGTAGGGCTCAACTCTCGCGTCGATATCCCATGACTTTTCCGCTTCAACTGTC 200
QY 202 C 202
DB 201 C 201
RESULT 7
AAH84099
ID AAH84099 standard; DNA; 487 BP.
XX AC AAH84099;
XX XX
XX DT 25-SEP-2001 (first entry)
XX XX
XX DE Mouse olfactory receptor encoding gene 6.
XX XX
XX KM Olfactory receptor; primate; mouse; human; food processing industry;
XX KM aromas; perfumery; toxic substance; ds.
XX OS Mus musculus domesticus.
XX PN WO200146262-A2.

```

```

XX PD 28-JUN-2001.
XX XX
XX PF 22-DEC-2000; 2000WO-IB002017.
XX PR 22-DEC-1999; 99US-0171746P.
XX PR 21-DEC-2000; 2000US-00747155.
XX XX
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Rouquier S, Giorgi D;
XX DR WPI; 2001-381911/40.
XX DR P-PSDB; AAG98584.
XX XX
XX PT Nucleic acids encoding primate and murine olfactory receptors, useful for
XX PT analysis odors e.g. in food processing and perfumery.
XX PS Claim 1; Page 415-416; 482pp; English.
XX XX
XX CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
XX CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
XX CC primate species, mouse and human. The nucleic acids and receptors may be
XX CC used in the food processing industry (e.g. for the detection of aromas,
XX CC quality control and sample analysis), in perfumery (e.g. for the analysis
XX CC or comparison of perfumes) and in the environment (e.g. for the detection
XX CC of toxic substances and/or trapping of odours)
XX SQ
SQ Sequence 487 BP; 86 A; 120 C; 105 G; 176 T; 0 U; 0 Other;
Query Match 5.9%; Score 57; DB 4; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.9e-18;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 514 CAACCTTGCACTACATGATGTGACATCCCTCCCTTGAGTCTCTGCAA 570
DB 145 CAACCTTGCACTACATGATGTGACATCCCTCCCTTGAGTCTCTGCAA 201
RESULT 8
AAH84095
ID AAH84095 standard; DNA; 486 BP.
XX AC AAH84095;
XX XX
XX DT 25-SEP-2001 (first entry)
XX XX
XX DE Mouse olfactory receptor encoding gene 2.
XX XX
XX KM Olfactory receptor; primate; mouse; human; food processing industry;
XX KM aromas; perfumery; toxic substance; ds.
XX OS Mus musculus domesticus.
XX PN WO200146262-A2.
XX PD 28-JUN-2001.
XX XX
XX PF 22-DEC-2000; 2000WO-IB002017.
XX PR 22-DEC-1999; 99US-0171746P.
XX PR 21-DEC-2000; 2000US-00747155.
XX XX
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Rouquier S, Giorgi D;
XX DR WPI; 2001-381911/40.
XX DR P-PSDB; AAG98580.
XX XX
XX PT Nucleic acids encoding primate and murine olfactory receptors, useful for
XX PT analysis odors e.g. in food processing and perfumery.
XX PN WO200146262-A2.

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PS Claim 1; Page 405-406; 482pp; English.

XX CC The invention relates to olfactory receptors (AG98432-AG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)

SQ Sequence 486 BP; 92 A; 114 C; 105 G; 175 T; 0 U; 0 Other;

QY Query Match 4.0%; Score 39; DB 4; Length 486;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 642 TTTTATCTCTTATGCTTTATCTTCCAGCATTTCTCC 680
 273 TTTTATCTCTTATGCTTTATCTTCCAGCATTTCTCC 311

RESULT 9
 AAH84062
 ID AAH84062 standard; DNA; 487 BP.
 XX AC
 XX AAH84062;
 DT 25-SEP-2001 (first entry)

DE Pongo pygmaeus olfactory receptor pseudogene 10.
 XX KM
 XX Olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance; ds.
 OS Pongo pygmaeus.
 PN WO200146262-A2.
 XX PD
 XX 28-JUN-2001.
 PF 22-DEC-2000; 2000WO-1B002017.
 XX PR
 XX 22-DEC-1999; 99US-0171746P.
 PR 21-DEC-2000; 2000US-00747155.
 XX PA
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX PI
 XX Rouquier S, Giorgi D;
 DR WPI; 2001-381911/40.
 XX PT
 XX Nucleic acids encoding primate and murine olfactory receptors, useful for
 PT analysis odors e.g. in food processing and perfumery.
 PS Claim 1; Page 347-348; 482pp; English.

XX CC The invention relates to olfactory receptors (AG98432-AG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)

SQ Sequence 487 BP; 88 A; 118 C; 107 G; 174 T; 0 U; 0 Other;

QY Query Match 4.0%; Score 39; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 642 TTTTATCTCTTATGCTTTTATCTTCCAGCATTTCTCC 680
 273 TTTTATCTCTTATGCTTTTATCTTCCAGCATTTCTCC 311

RESULT 10
 AAH84089
 ID AAH84089 standard; DNA; 487 BP.
 XX AC
 XX AAH84089;
 DT 25-SEP-2001 (first entry)

DE Salmiiri boliviensis olfactory receptor encoding gene 11.
 XX KM
 XX Olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance; ds.
 OS Salmiiri boliviensis.
 PN WO200146262-A2.
 XX PD
 XX 28-JUN-2001.
 PF 22-DEC-2000; 2000WO-1B002017.
 XX PR
 XX 22-DEC-1999; 99US-0171746P.
 PR 21-DEC-2000; 2000US-00747155.
 XX PA
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX PI
 XX Rouquier S, Giorgi D;
 DR WPI; 2001-381911/40.
 DR P-PsDB; AG98575.
 XX PT
 XX Nucleic acids encoding primate and murine olfactory receptors, useful for
 PT analysis odors e.g. in food processing and perfumery.
 PS Claim 1; Page 394-395; 482pp; English.

XX CC The invention relates to olfactory receptors (AG98432-AG98609) and the
 CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
 CC primate species, mouse and human. The nucleic acids and receptors may be
 CC used in the food processing industry (e.g. for the detection of aromas,
 CC quality control and sample analysis), in perfumery (e.g. for the analysis
 CC or comparison of perfumes) and in the environment (e.g. for the detection
 CC of toxic substances and/or trapping of odours)

SQ Sequence 487 BP; 92 A; 116 C; 105 G; 174 T; 0 U; 0 Other;

QY Query Match 4.0%; Score 39; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 5.6e-09;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 642 TTTTATCTCTTATGCTTTTATCTTCCAGCATTTCTCC 680
 273 TTTTATCTCTTATGCTTTTATCTTCCAGCATTTCTCC 311

RESULT 11
 AAH84050
 ID AAH84050 standard; DNA; 489 BP.
 XX AC
 XX AAH84050;
 DT 25-SEP-2001 (first entry)

DE Macaca sylvanus olfactory receptor pseudogene 6.
 XX KM
 XX Olfactory receptor; primate; mouse; human; food processing industry;
 KM aromas; perfumery; toxic substance; ds.
 OS Macaca sylvanus.
 PN WO200146262-A2.

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XX 28-JUN-2001.
PD
PF 22-DEC-2000; 2000WO-IB002017.
XX
XX 22-DEC-1999; 99US-0171746P.
PR 21-DEC-2000; 2000US-00747155.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI Rouquier S, Giorgi D;
XX WPI; 2001-381911/40.
DR
XX Nucleic acids encoding primate and murine olfactory receptors, useful for
PT analysis odors e.g. in food processing and perfumery.
XX
PS Claim 1; Page 326; 482pp; English.
XX
XX The invention relates to olfactory receptors (AAG98432-AAG98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours)
XX
SQ Sequence 489 BP; 95 A; 120 C; 104 G; 170 T; 0 U; 0 Other;

Query Match
Best Local Similarity 4.0%; Score 39; DB 4; Length 489;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTATGAGTTTATCTTTCAGCATTCCTCC 680
DB 273 TTTTATCTCTATGAGTTTATCTTTCAGCATTCCTCC 311

RESULT 12
AAH84069
ID AAH84069 standard; DNA; 491 BP.
XX
AC AAH84069;
XX
DT 25-SEP-2001 (first entry)
XX
DE Pongo pygmaeus olfactory receptor pseudogene 13.
XX
KM Olfactory receptor; primate; mouse; human; food processing industry;
XX aromas; perfumery; toxic substance; ds.
OS
XX Pongo pygmaeus.
XX WO200146262-A2.
XX
XX 28-JUN-2001.
XX
XX 22-DEC-2000; 2000WO-IB002017.
XX
XX 22-DEC-1999; 99US-0171746P.
XX 21-DEC-2000; 2000US-00747155.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Rouquier S, Giorgi D;
XX WPI; 2001-381911/40.
XX
XX Nucleic acids encoding primate and murine olfactory receptors, useful for
PT analysis odors e.g. in food processing and perfumery.
XX
PS Claim 1; Page 357-358; 482pp; English.
XX

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CC The invention relates to olfactory receptors (AAG98432-AAG98609) and the
CC genes encoding them (AAH83879-AAH84131) including pseudogenes of 10
CC primate species, mouse and human. The nucleic acids and receptors may be
CC used in the food processing industry (e.g. for the detection of aromas,
CC quality control and sample analysis), in perfumery (e.g. for the analysis
CC or comparison of perfumes) and in the environment (e.g. for the detection
CC of toxic substances and/or trapping of odours)
XX
SQ Sequence 491 BP; 92 A; 118 C; 105 G; 176 T; 0 U; 0 Other;

Query Match
Best Local Similarity 4.0%; Score 39; DB 4; Length 491;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 642 TTTTATCTCTATGAGTTTATCTTTCAGCATTCCTCC 680
DB 273 TTTTATCTCTATGAGTTTATCTTTCAGCATTCCTCC 311

RESULT 13
AAH32421
ID AAH32421 standard; DNA; 930 BP.
XX
AC AAH32421;
XX
DT 30-JUL-2001 (first entry)
XX
DE Human olfactory receptor polynucleotide, SEQ ID NO: 994.
XX
XX Human; olfactory receptor; OR; primary scent determination;
XX secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation; ds.
OS
XX Homo sapiens.
XX
XX WO200127158-A2.
XX
XX 19-APR-2001.
XX
XX 06-OCT-2000; 2000WO-US027582.
XX
XX 08-OCT-1999; 99US-0156615P.
XX 24-FEB-2000; 2000US-0184809P.
XX
XX (DIGI-) DIGISCENTS.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX
XX New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
XX Claim 8; Page 577; 1857pp; English.
XX
XX The present sequence is one of a number of isolated polynucleotides which
CC encode polypeptides involved in olfactory sensation. The polynucleotides
CC can be used in screening for olfactory agonists and antagonists. The
CC methods allow for the determination of primary scents and the
CC identification of the odour receptors used to detect these primary
CC scents. The methods also enable determination of secondary scents and the
CC identification of combinations of odour receptors that are involved in
CC detecting such secondary scents. This enables the construction of a scent
CC representation (also called a scent fingerprint or scent profile), which
CC may be used to re-create and edit scents. Libraries of olfactory
CC receptors are useful for determining the interaction pattern of a
CC composition with the receptors, and can be used for determining
CC differences in the olfactory faculties of different individuals
XX
SQ Sequence 930 BP; 190 A; 251 C; 188 G; 301 T; 0 U; 0 Other;

Query Match
4.0%; Score 39; DB 4; Length 930;

```

CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological disorders (e.g. epilepsy, stroke, schizophrenic disorders and neuroskeletal disorders), cardiovascular disorders (e.g. hypertension, CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia, CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus, CC osteoporosis, psoriasis), and metabolic disorders such as obesity. CC Furthermore, the polynucleotide is useful as primers for detecting CC single nucleotide polymorphisms; as elements in microarray, to monitor or CC measure protein-protein interactions, drug-target interactions, and gene CC expression profiles; to generate a transcript image of a tissue or cell CC type, and to generate hybridisation probes useful in mapping the CC naturally occurring genomic sequence. This sequence encodes G-protein CC coupled receptor 14, one of 21 GPCR proteins described in the method of CC the invention

XX Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;

Qy Query Match 4.0%; Score 39; DB 5; Length 933;
Best Local Similarity 100.0%; Pval. No. 5.7e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 235 TCCCAAAATGCTGATGATTTTGTCTCAAGAGAAACAT 273
|||||
231 TCCCAAAATGCTGATGATTTTGTCTCAAGAGAAACAT 269

RESULT 15
AAS42233
ID AAS42233 standard; cDNA; 933 BP.

AC AAS42233;
XX
XX 18-DEC-2001 (first entry)
DT
XX
DE Human cDNA encoding olfactory receptor AORF26.
KW
XX Human: olfactory receptor; G protein-coupled receptor; GPCR; odourant;
KM ses; food additive; cosmetic; fragrance; pharmaceutical additive.
OS Homo sapiens.
XX
XX MO200168805-A2.
XX
XX 20-SEP-2001.
PD
XX
XX 13-MAR-2001; 2001WC-US007771.
FF
XX
XX 13-MAR-2000; 2000US-0188914P.
PR
XX 24-MAR-2000; 2000US-0192033P.
PR
XX 12-APR-2000; 2000US-0198474P.
PR
XX 24-APR-2000; 2000US-0199335P.
PR
XX 26-MAY-2000; 2000US-0207702P.
PR
XX 23-JUN-2000; 2000US-0218449P.
PR
XX 16-AUG-2000; 2000US-0226534P.
PR
XX 07-SEP-2000; 2000US-0230732P.
PR
XX 07-FEB-2001; 2001US-0266862P.

PA (SENO-) SENOMYX INC.
XX
PL Zozulya S;
XX
DR WPI; 2001-570867/64.
XX
DR P-PSDB; AAU24540.
XX
XX Nucleic acids encoding human olfactory G protein-coupled receptors, where
PT useful for screening for compounds involved in olfactory sensation, where
PT the compounds can be used in the food, pharmaceutical and cosmetic
PT industries to customize odors.

PS Claim 1; Page 94; 319pp; English.
XX
XX
CC The invention relates to nucleic acids encoding human olfactory
CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's

CC specifically recognise molecules, odourants, that elicit specific
 CC olfactory sensation. The human olfactory receptors and polynucleotides
 CC encoding them are useful for screening a library of chemical compounds
 CC for compounds that are involved in olfactory sensation. Modulators of
 CC their activity are useful for pharmacological and genetic modulation of
 CC olfactory signalling pathways. Therefore, they can be used in the food,
 CC pharmaceutical and cosmetic industries to customise odours and
 CC fragrances. The present sequence encodes a human olfactory receptor of
 the invention

XX
 SQ Sequence 933 BP; 192 A; 251 C; 188 G; 302 T; 0 U; 0 Other;

Query Match 4.0%; Score 39; DB 5; Length 933;
 Best Local Similarity 100.0%; Pred. No. 5.7e-09;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAACAT 273
 Db 231 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAACAT 269

Search completed: September 30, 2004, 06:13:28
 Job time : 4/74 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 05:28:10 ; Search time 94 Seconds
(without alignments)
5685.295 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 aatgctgcgcgagaactcctt.....ttttagaacaagaaagaga 963

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 20

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	224	23.3	485	4	US-09-621-976-18883
					Sequence 18883, A

ALIGNMENTS

RESULT 1
US-09-621-976-18883/C
Sequence 18883 Application US/09621976
Patent No. 6635063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18883
LENGTH: 485
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-18883

Query Match

23.3% ; Score 224 ; DB 4 ; Length 485 ;

Best Local Similarity 100.0% ; Pred. No. 6.1e-104 ;
Matches 224 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY	402	TCACCATGCTCTCCCGACGCTGTGTTGCTCCTTTTACTGCGGTGTCTACGCGATGGGGCTTT	461
DB	265	TCACCATGCTCTCCCGACGCTGTGTTGCTCCTTTTACTGCGGTGTCTACGCGATGGGGCTTT	206
QY	462	TTGGGGCTGTGGGCTCATACAGAAATATAGTTTCTCACCTTTTGTGACAGACCTTG	521
DB	205	TTGGGGCTGTGGGCTCATACAGAAATATAGTTTCTCACCTTTTGTGACAGACCTTG	146
QY	522	TCATCACTACATGTGTGACATCCTTCCCTTTTGAGCTCTCTGCAACGCTTTTACA	581
DB	145	TCATCACTACATGTGTGACATCCTTCCCTTTTGAGCTCTCTGCAACGCTTTTACA	86
QY	582	TAAATGCTGTCATCTTATTTGTTGTGACCGTTCATTTGG	625
DB	85	TAAATGCTGTCATCTTATTTGTTGTGACCGTTCATTTGG	42

Search completed: September 30, 2004, 08:16:09
Job time : 95 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 30, 2004, 04:40:49 ; Search time 3087 seconds

(without alignments)
9315.607 Million cell updates/sec

Title: US-10-023-597-23

Perfect score: 963
Sequence: 1 aatggctgcgcgagaactct.....ttttagaacaagaagaaga 963

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 20

Total number of hits satisfying chosen parameters: 201

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_estbu:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	4.0	799	29	AY407110 Pan trogl
2	39	4.0	933	29	AY407109 Homo sapi
3	33	3.4	903	29	AY405609 Homo sapi
4	31	3.2	605	14	CB174014 OR_2031G0

5	30	3.1	504	14	CB174105	CB174105 OR_2034C0
6	28	2.9	456	12	B1274717	B1274717 UI-R-CX0-
7	28	2.9	560	14	CB173336	CB173336 OR_2016G0
8	28	2.9	683	28	A0931094	A0931094 RPCI-23-2
9	26	2.7	442	14	CA881328	CA881328 K0989F04-
10	26	2.7	472	14	CA880338	CA880338 K0982C03-
11	26	2.7	492	28	B04945	B04945 GSRU-S0F-U-
12	26	2.7	877	28	BH418698	BH418698 B0GT281TF
13	26	2.7	903	29	AY405611	AY405611 Mus muscu
14	26	2.7	933	29	AY407111	AY407111 Mus muscu
15	25	2.6	625	29	CE158635	CE158635 tigr-gss-
16	24	2.5	504	29	CE243689	CE243689 tigr-gss-
17	24	2.5	683	13	B1720370	B1720370 BY720370
18	24	2.5	899	29	AY405610	AY405610 Pan trogl
19	23	2.4	222	10	BF444685	BF444685 262681 MA
20	23	2.4	334	10	AM486191	AM486191 71360 MAR
21	23	2.4	359	13	BY024438	BY024438 OR_2021H0
22	23	2.4	387	14	CB173998	CB173998 OR_2021H0
23	23	2.4	387	28	B2949576	B2949576 CH240_380
24	23	2.4	392	14	CB173314	CB173314 OR_201ED1
25	23	2.4	451	12	B1399100	B1399100 MT-PAT1-
26	23	2.4	455	28	AZ806221	AZ806221 2M068E10
27	23	2.4	475	28	AZ016145	AZ016145 RPCI-23-3
28	23	2.4	496	14	AM431124	AM431124 71365 MAR
29	23	2.4	652	14	CB440691	CB440691 690988 MA
30	23	2.4	931	28	CNS07890	AL434184 T3 end of
31	23	2.4	962	29	CNS07761	AL432287 T3 end of
32	23	2.4	985	29	CNS07981	AL435059 T7 end of
33	23	2.4	1066	29	CNS076WC	AL431938 T3 end of
34	23	2.4	1201	9	AL539244	AL539244 T3 end of
35	22	2.3	259	13	B0451234	B0451234 PESTroab0
36	22	2.3	267	10	B8049231	B8049231 OR_2019B0
37	22	2.3	394	14	CB173920	CB173920 OR_2019B0
38	22	2.3	414	13	B0451187	B0451187 PESTroab0
39	22	2.3	423	13	B0577021	B0577021 PESTroab1
40	22	2.3	432	12	B1670687	B1670687 PESTroab1
41	22	2.3	445	14	CB173642	CB173642 OR_2022B0
42	22	2.3	454	14	CB173295	CB173295 OR_2014G0
43	22	2.3	463	13	B0498696	B0498696 PESTroac0
44	22	2.3	473	14	CB173023	CB173023 OR_204803
45	22	2.3	535	13	B0497196	B0497196 PESTroab5

ALIGNMENTS

RESULT 1
AY407110
LOCUS
DEFINITION Pan troglodytes OREB12 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY407110.1 GI:39763081
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
TITLE
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
2 (bases 1 to 799)
REFERENCE
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..799

gene /organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

<1..>799

/gene="OR8B12"

/locus_tag="HGM2781"

ORIGIN

Query Match 4.0%; Score 39; DB 29; Length 799;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAACAT 273

Db 231 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAACAT 269

RESULT 2

AY407109 933 bp DNA linear GSS 15-DEC-2003

LOCUS Homo sapiens OR8B12 gene, VIRTUAL TRANSCRIPT, partial sequence,

DEFINITION genomic survey sequence.

ACCESSION AY407109.1 GI:39763080

VERSION AY407109.1 GI:39763080

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 933)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PubMed 14671302

2 (bases 1 to 933)

REFERENCE 1 (bases 1 to 933)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..933

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>933

/gene="OR8B12"

/locus_tag="HGM2781"

ORIGIN

Query Match 4.0%; Score 39; DB 29; Length 933;

Best Local Similarity 100.0%; Pred. No. 6.9e-09;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 235 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAACAT 273

Db 231 TCCCAAAATGCTGATGAGTTTGTCTCAAGAGAACAT 269

RESULT 3

AY405609 903 bp DNA linear GSS 16-DEC-2003

LOCUS Homo sapiens OR8B8 gene, VIRTUAL TRANSCRIPT, partial sequence,

DEFINITION genomic survey sequence.

ACCESSION AY405609.1 GI:39761583

VERSION AY405609

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 903)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PubMed 14671302

2 (bases 1 to 903)

REFERENCE 1 (bases 1 to 903)

AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smitsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..903

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

<1..>903

/gene="OR8B8"

/locus_tag="HGM2281"

ORIGIN

Query Match 3.4%; Score 33; DB 29; Length 903;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 527 CACTACATGTGTGACATCCTTCCCTCTTGTAG 559

Db 493 CACTACATGTGTGACATCCTTCCCTCTTGTAG 525

RESULT 4

CB174014 605 bp mRNA linear EST 09-OCT-2003

LOCUS OR 2031G09.010529.y1 Adult mouse olfactory epithelium library Mus

DEFINITION musculus cDNA clone 2031G09 5', mRNA sequence.

ACCESSION CB174014.1 GI:37592643

VERSION CB174014.1 GI:37592643

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 605)

AUTHORS Young,J.K., Shykhet,B.M., Lane,R.P., Tonnes-Priddy,L., Ross,J.A., Walker,M., Williams,E.M. and Traak,B.J.

TITLE Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels

JOURNAL Genome Biol. 4 (11), R71.1-R71.15 (2003)

CONTACT: Young JM

Trask Lab, Division of Human Biology

Fred Hutchinson Cancer Research Center

1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA

98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@hrc.org
Young gene new name GA_X6K02T2PVT-32841223-32842158
Young gene old name GA_X5J8B7M60AJ-489886-489950
Other gene name K9
Zhang gene name MOR171-6
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
1..605
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2031G09"
/cisse_type="olfactory and respiratory epithelium"
/dev_stage="adult"
/clone_lib="Adult mouse olfactory epithelium library"
/note="Organ: Olfactory turbinates; Vector: LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library was provided by Leslie Voeshall. mRNA was prepared from the olfactory and respiratory epithelium of an adult mouse. Oligo-dT primed cDNA was directionally cloned into Stratagene's LambdaZAPII-XR vector."

ORIGIN

Query Match 3.2%; Score 31; DB 14; Length 605;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 863 TTATCTACAGCCTGAGGATTAAGATGTCA 893
DB 504 TTATCTACAGCCTGAGGATTAAGATGTCA 534

RESULT 5

CB174105 504 bp mRNA linear EST 09-OCT-2003
LOCUS OR_2034C01.010615.y1 Adult mouse olfactory epithelium library Mus
DEFINITION musculus cDNA clone 2034C01 5', mRNA sequence.
CB174105
VERSION CB174105.1 GI:37592734
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 504)
Young, J.M., Shykind, B.M., Lane, R.P., Tonnes-Priddy, L., Ross, J.A., Walker, M., Williams, E.M. and Trask, B.J.

ORFANT: receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels

Genome Biol. 4 (11), R71.1-R71.15 (2003)

unequal expression levels

Contact: Young JM

Trask Lab, Division of Human Biology

Fred Hutchinson Cancer Research Center

1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA

98109-1024, USA

Tel: 206 667 1471

Fax: 206 667 6524

Email: jayoung@hrc.org

Young gene new name GA_X6K02T2PVT-33470347-33469403

Young gene old name GA_X5J8B7M3MPH-108802-107858

Zhang gene name MOR171-15

Seq primer: M13 Reverse.

Location/Qualifiers

1..504
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2034C01"
/tissue_type="Olfactory and respiratory epithelium"

ORIGIN

Query Match 3.1%; Score 30; DB 14; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGATTAAGATGTCAA 895
DB 342 ATCTACAGCCTGAGGATTAAGATGTCAA 371

RESULT 6

B1274717/c 456 bp mRNA linear EST 18-JUN-2001
LOCUS UI-R-CX0-bxd-b-11-0-UI.s1 UI-R-CX0 Rattus norvegicus cDNA clone
DEFINITION UI-R-CX0-bxd-b-11-0-UI 3', mRNA sequence.
B1274717
VERSION B1274717.1 GI:14885894
KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 456)

Bonaldi, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: bento-soares@uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized rat placenta pool library cDNA library preparation: M.B. Soares Lab Gene distribution: clones will be available through Research Gene Services (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-48,
>AT rich#low complexity
Seq primer: M13 Forward
POLY-A=yes.

FEATURES

source

Location/Qualifiers
1..456
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CX0-bxd-b-11-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CX0"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CX0 library is a normalized library constructed from the following rat placenta tissues: embryonic day 17, embryonic day 19, embryonic day 21. For a detailed

description of the library from which this clone was derived, please visit our web site at rtest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG TISSUE=rat placenta pool
TAG_LIB=UI-R-CX0
TAG_SEQ=TCACGACAGT"

ORIGIN

Query Match 2.9%; Score 28; DB 12; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGATTAAGATGTCA 893
DB 303 ATCTACAGCCTGAGGATTAAGATGTCA 276

RESULT 7
CB173336
LOCUS
DEFINITION OR2016G01.C04_001130_27.Y1 Adult mouse olfactory epithelium
library Mus musculus cDNA clone 2016G01 5', mRNA sequence.
CB173336
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 560)
Walker, M., Williams, E.M., Lane, R.P., Tomnes-Priddy, L., Ross, J.A., Odorant receptor expressed sequence tags demonstrate olfactory expression of over 400 genes, extensive alternate splicing and unequal expression levels
Genome Biol. 4 (11), R71.1-R71.15 (2003)
Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA 98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org

Young gene new name GA_X6K0272PMTD-32935684-32934749

Young gene old name GA_X5J8B7MSU54-727-5

Young gene old name GA_X5J8B7M60AJ-401357-402240

Other gene name K4

Zhang gene name MOR171-32P

Zhang gene name MOR171-41P

Seg primer: M13 Reverse.

Location/Qualifiers

1..560

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="2016G01"

/tissue_type="Olfactory and respiratory epithelium"

/dev_stage="Adult"

/clone_lib="Adult mouse olfactory epithelium library"

/note="Organ: Olfactory turbinates; Vector: LambdaZAPII-XR; Site_1: EcoRI; Site_2: XhoI; This library was provided by Leslie Vossahl. mRNA was prepared from the olfactory and respiratory epithelium of an adult mouse. Oligo-dT primed cDNA was directionally cloned into Stratagene's lambdaZAPII-XR vector."

ORIGIN

Query Match 2.9%; Score 28; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGATTAAGATGTCA 893
DB 327 ATCTACAGCCTGAGGATTAAGATGTCA 354

RESULT 8

LOCUS

AO931094 683 bp DNA linear GSS 21-DEC-1999
RPCI-23-283118.TV RPCI-23 Mus musculus genomic clone
RPCI-23-283118, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Other GSSs: RPCI-23-283118.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@jmg.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea Ch Genetics (<http://resgen.com>). BAC end page: http://www.tigr.org/tdb/bac_end/mouse/bac_end_intro.html
plate: 283 row: L column: 18
Seg primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..683

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-283118"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Site selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 2.9%; Score 28; DB 28; Length 683;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 ATCTACAGCCTGAGGATTAAGATGTCA 893
DB 71 ATCTACAGCCTGAGGATTAAGATGTCA 98

RESULT 9

LOCUS

CA881328/c 444 bp mRNA linear EST 20-DEC-2002
DEFINITION K0989F04-5N NTA Mouse Neural Stem Cell (Undifferentiated) cDNA

Library (Long) Mus musculus cDNA clone NIA:K0989F04 IMAGE:30092799
5', mRNA sequence.
ACCESSION CA881328
VERSION CA881328.1 GI:27332877
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 444)
AUTHORS Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alpa, K., Vescovi, A.L. and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)
JOURNAL Unpublished (2002)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0989 row: F column: 04
Seq primer: -21M13 Reverse
High quality sequence stop: 444
POLYA-No.

Location/Qualifiers
1..444
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD1"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="NIA:K0989F04 IMAGE:30092799"
/dev_stage="Adult"
/lab_host="DH108"
/clone_lib="NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11:1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGATGTTCTAGATCGAGCGCCCTTTTCTTTT-3'] from 2.0 Microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker LL-Sa14, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH108 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 kb. The library was constructed by Yulan Piao."

ORIGIN
Query Match 2.7%; Score 26; DB 14; Length 444;
Best Local Similarity 100.0%; Pred.No.0.053;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 545 CTTCCTCTTGTAGCTCTCTGCAA 570
DB 388 CTTCCTCTTGTAGCTCTCTGCAA 363

RESULT 10
CA880338/c 472 bp mRNA linear EST 20-DEC-2002

K0982C03-5N NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long) Mus musculus cDNA clone NIA:K0982C03 IMAGE:30092090
5', mRNA sequence.
ACCESSION CA880338
VERSION CA880338.1 GI:27331887
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 472)
AUTHORS Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alpa, K., Vescovi, A.L. and Ko, M.S.H.
TITLE Systematic Analyses of NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)
JOURNAL Unpublished (2002)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0982 row: C column: 03
Seq primer: -21M13 Reverse
High quality sequence stop: 472
POLYA-No.

Location/Qualifiers
1..472
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD1"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="NIA:K0982C03 IMAGE:30092090"
/dev_stage="Adult"
/lab_host="DH108"
/clone_lib="NIA Mouse Neural Stem Cell (Undifferentiated) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11:1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGATGTTCTAGATCGAGCGCCCTTTTCTTTT-3'] from 2.0 Microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker LL-Sa14, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH108 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.8 kb. The library was constructed by Yulan Piao."

ORIGIN
Query Match 2.7%; Score 26; DB 14; Length 472;
Best Local Similarity 100.0%; Pred.No.0.052;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 545 CTTCCTCTTGTAGCTCTCTGCAA 570
DB 388 CTTCCTCTTGTAGCTCTCTGCAA 363

RESULT 11
B04945/c

LOCUS B04945 492 bp DNA linear GSS 13-JUL-1996
 DEFINITION CSR1-50F8-u CSR1 flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone CSR1-50F8, genomic survey sequence.
 ACCESSION B04945
 VERSION B04945.1 GI:1414223
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 492)
 Evans, G.A., Burbee, D., Davies, C., Hahner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M., Kufner, K. and Garner, H. R.
 Genomic Sequence Sampled Map of Chromosome 11
 Unpublished (1996)
 CONTACT: Evans GA, Shane Probst
 McDermott Center for Human Growth and Development
 University of Texas Southwestern Medical Center At Dallas
 5323 Harry Hines Blvd, Dallas TX 75235-8591
 Tel: 214-648-1600
 Fax: 214-648-1666
 Email: g.evans@utsw.swned.edu, shanemcdermott.swned.edu
 PCR Primers
 FORWARD: GACTAGAGAGAGAAAATGCG
 BACKWARD: TTATCTCAATTGTGCTTC
 Seq primer: T7
 Class: cosmid ends
 High quality sequence stop: 492.
 Location/Qualifiers
 1..492
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="CSR1-50F8"
 /sex="female"
 /cell_type="chimeric hamster somatic cell hybrid"
 /clone_11b="CSR1 flow sorted Chromosome 11 specific cosmid"
 /note="Vector: sCos-1; Human Chromosome 11 specific cosmid library prepared from flow sorted human Chromosome 11 derived from Chinese Hamster Ovary (CHO) monochromosomal somatic cell hybrid, J1"

ORIGIN
 Query Match 2.7%; Score 26; DB 28; Length 492;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 233 ATTCCCAAAATGCTGATGATTGTTTGT 258
 ||||||||||||||||||||||||||||||||
 137 ATTCCCAAAATGCTGATGATTGTTTGT 112

RESULT 12
 BH418698/c 877 bp DNA linear GSS 12-DEC-2001
 LOCUS BH418698
 DEFINITION BOGT281TR BOGT Brassica oleracea genomic clone BOGT281, genomic survey sequence.
 ACCESSION BH418698
 VERSION BH418698.1 GI:17604426
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 877)
 Town, C.D., Van Aken, S., Utehrack, T., Koo, H. and Fraser, C.M.
 Whole genome shotgun sequencing of Brassica oleracea
 Unpublished (2001)
 Other_GSSs: BOGT281TR

CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.
 Location/Qualifiers
 1..877
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO:000DH3"
 /db_xref="taxon:3712"
 /clone="BOGT281"
 /note="Vector: pBOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pBOS1 using BstXI linkers"

ORIGIN
 Query Match 2.7%; Score 26; DB 28; Length 877;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 307 CTTCTCTGTTCTTTGTTGTTTCTTG 332
 ||||||||||||||||||||||||||||||||
 118 CTTCTCTGTTCTTTGTTGTTTCTTG 93

RESULT 13
 AY405611 903 bp DNA linear GSS 16-DEC-2003
 LOCUS AY405611
 DEFINITION Mus musculus OR888 gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.
 ACCESSION AY405611
 VERSION AY405611.1 GI:39761585
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 903)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriter, S., Wang, G., Zheng, X.H., White, T.D., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL PUBMED 14671302
 2 (bases 1 to 903)
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriter, S., Wang, G., Zheng, X.H., White, T.D., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering them based on alignment.
 Location/Qualifiers
 1..903
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /gene="OR888"
 /locus_tag="HMCW281"

ORIGIN
 Query Match 2.7%; Score 26; DB 29; Length 903;
 Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TCTTCTTCCTGTTTCTAGGTTCTAC 106
 47 TCTTCTTCCTGTTTCTAGGTTCTAC 72

RESULT 14
 AY407111 933 bp DNA linear GSS 15-DEC-2003
 LOCUS Mus musculus OR6B12 gene, VIRUTAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY407111
 VERSION AY407111.1 GI:39763082
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 933)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
 Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene titros
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 2 (bases 1 to 933)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
 Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES
 Location/Qualifiers
 source 1..933
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
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 /gene="OR6B12"
 /locus_tag="HMC2781"

ORIGIN
 Query Match 2.7%; Score 26; DB 29; Length 933;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 CTTCCCTTCTTGTAGCTCTCTGCAA 570
 541 CTTCCCTTCTTGTAGCTCTCTGCAA 566

RESULT 15
 CE158635 626 bp DNA linear GSS 25-SEP-2003
 LOCUS tigr-gss-dog-17000371402682 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE158635
 VERSION CE158635.1 GI:35286025
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 625)
 Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.

TITLE The dog genome: survey sequencing and comparative analysis
 JOURNAL Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627

COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Class: Shotgun.
 Location/Qualifiers
 source 1..625
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 2.6%; Score 25; DB 29; Length 625;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 TCTTCTTCCTGTTTCTAGGTTCTCA 105
 162 TCTTCTTCCTGTTTCTAGGTTCTCA 186

Search completed: September 30, 2004, 08:14:33
 Job time : 3092 secs

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